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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:21:04 ; Search time 37.825 Seconds
(without alignments)
59,888 Million cell updates/sec

Title: US-09-821-380-1

Perfect score: 86

Sequence: 1 MTRVLQGLPALPQWVC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : A_Geneseq_101002.*
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23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	17	AAU08736	Human immunoregulator
2	86	100.0	20	AAU08736	38-57 region of hu
3	86	100.0	20	AAU08736	Peptide similar to
4	86	100.0	20	AAU08736	HCG antigenic pept
5	86	100.0	20	AAU08736	Human hCG beta-sub
6	86	100.0	20	AAU08736	Human chorionic go
7	86	100.0	20	AAU08736	Peptide containing
8	86	100.0	20	AAU08736	Human Chorionic Go
9	86	100.0	20	AAU08736	Human Chorionic Go
10	86	100.0	20	AAU08736	Structure XXVII (p

ALIGNMENTS

RESULT 1

AAU08736

ID AAU08736 standard; Peptide; 17 AA.

XX AAU08736;

AC AAU08736;

XX 19-DEC-2001 (first entry)

XX Human immunoregulator functional fragment peptide #1.

XX Immunoregulator; human; beta-human chorionic gonadotropin; beta-HCG;
XX inflammation; multiple sclerosis; diabetes; anaphylactic shock; asthma;
XX pregnancy related disorder; pre-eclampsia; autoimmune disease; allergy;

11	86	100.0	20	22	AAU49904	Human chorionic go
12	86	100.0	22	8	AAU71013	Sequence of fragme
13	86	100.0	24	22	AAU64086	Human Clara cell p
14	86	100.0	25	22	AAU64108	Human Clara cell p
15	86	100.0	27	22	AAU01181	Human chorionic go
16	86	100.0	60	10	AAU91836	Beta subunit of hu
17	86	100.0	85	20	AAU95536	Human chorionic go
18	86	100.0	93	22	AAU04621	Human chorionic go
19	86	100.0	93	22	AAU04493	Human chorionic go
20	86	100.0	111	12	AAU15161	HCG deletion mutan
21	86	100.0	114	14	AAU31003	Modified hCG beta-
22	86	100.0	114	14	AAU31005	Modified hCG beta-
23	86	100.0	114	17	AAU88920	HCG analogue-G bet
24	86	100.0	114	17	AAU88921	HCG analogue-DG' b
25	86	100.0	114	17	AAU88922	HCG analogue-Q bet
26	86	100.0	114	22	AAU04620	Human chorionic go
27	86	100.0	114	22	AAU04492	Human chorionic go
28	86	100.0	115	12	AAU15078	HCG/hfsh chimera,
29	86	100.0	115	12	AAU15081	HCG/hfsh chimera,
30	86	100.0	115	12	AAU15083	HCG/hfsh chimera,
31	86	100.0	115	12	AAU15087	HCG/hfsh chimera,
32	86	100.0	116	12	AAU15162	HCG deletion mutan
33	86	100.0	116	12	AAU15172	HCG methionine sub
34	86	100.0	117	14	AAU31008	Modified hCG beta-
35	86	100.0	117	14	AAU31007	Modified hCG beta-
36	86	100.0	117	17	AAU88924	HCG analogue-GT be
37	86	100.0	117	17	AAU88925	HCG analogue-DGT b
38	86	100.0	118	12	AAU15070	HCG/hfsh chimera,
39	86	100.0	118	12	AAU15071	HCG/hfsh chimera,
40	86	100.0	122	12	AAU15108	HCG/bLH chimera, D
41	86	100.0	122	12	AAU15107	HCG/bLH chimera, D
42	86	100.0	122	12	AAU15119	HCG/hLH chimera, A
43	86	100.0	122	12	AAU15123	HCG/hLH chimera, A
44	86	100.0	123	12	AAU15096	HCG/hfsh chimera,
45	86	100.0	123	12	AAU15163	HCG deletion mutan
46	86	100.0	124	12	AAU15095	HCG/hfsh chimera,
47	86	100.0	132	19	AAU69449	Human chorionic go
48	86	100.0	133	12	AAU15164	HCG deletion mutan
49	86	100.0	137	12	AAU15165	HCG deletion mutan
50	86	100.0	138	12	AAU15088	HCG/hfsh chimera,
51	86	100.0	139	12	AAU15061	HCG/hfsh chimera,
52	86	100.0	139	12	AAU15167	HCG deletion mutan
53	86	100.0	140	21	AAU92000	Human chorionic go
54	86	100.0	142	20	AAU95526	Glycoprotein hormo
55	86	100.0	144	12	AAU15178	HCG histidine subs
56	86	100.0	144	12	AAU15093	HCG/hfsh chimera,
57	86	100.0	145	12	AAU15062	HCG/hfsh chimera,
58	86	100.0	145	12	AAU15066	HCG/hfsh chimera,
59	86	100.0	145	12	AAU15067	HCG/hfsh chimera,
60	86	100.0	145	12	AAU15068	HCG/hfsh chimera,
61	86	100.0	145	12	AAU15069	HCG/hfsh chimera,
62	86	100.0	145	12	AAU15072	HCG/hfsh chimera,
63	86	100.0	145	12	AAU15073	HCG/hfsh chimera,
64	86	100.0	145	12	AAU15174	HCG histidine subs
65	86	100.0	145	12	AAU15116	HCG/hLH chimera, A

KW rheumatoid arthritis; Sjogren's syndrome; graft-versus-host disease;
 KW thrombocytopenia; pernicious anaemia; Addison's disease; dermatomyositis;
 KW idiopathic leucopenia; primary biliary cirrhosis; cryptogenic cirrhosis;
 KW active chronic hepatitis; ulcerative colitis; polymyositis; scleroderma;
 KW mixed connective tissue disease; discoid lupus erythematosus; neotropic;
 KW antidiabetic; immunosuppressive; dermatological; antirheumatic; virucide;
 KW antithratic; antiasthmatic; anti-infertility; haemostatic;
 KW antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 PN EP1138692-A1.
 XX
 PD 04-OCT-2001.
 XX
 PF 29-MAR-2000; 2000EP-0201139.
 XX
 PR 29-MAR-2000; 2000EP-0201139.
 XX
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.
 XX
 PI Khan NA, Benner R;
 XX
 DR WPI; 2001-627804/73.
 XX
 PT Immunoregulator useful in the treatment of e.g. diabetes is obtained or
 PT derived from nicked beta-human chorionic gonadotropin -
 XX
 PS Claim 5; Page 18; 36pp; English.
 XX
 CC The invention relates to an immunoregulator obtained or derived from
 CC nicked beta-human chorionic gonadotropin (beta-HCG). The immunoregulator
 CC can be used in the treatment of immune-mediated disorders such as chronic
 CC inflammation (e.g. multiple sclerosis, diabetes), acute inflammation
 CC (e.g. septic or anaphylactic shock), pregnancy related immune-mediated
 CC disorders (e.g. pre-eclampsia), autoimmune disease (e.g. rheumatoid
 CC arthritis), allergy (e.g. asthma), Sjogren's syndrome, graft-versus-host
 CC disease, thrombocytopenia, pernicious anaemia, Addison's disease,
 CC idiopathic leucopenia, primary biliary cirrhosis, active chronic
 CC hepatitis, cryptogenic cirrhosis, ulcerative colitis, dermatomyositis,
 CC lupus erythematosus. This sequence represents a human immunoregulator
 CC functional fragment peptide.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 86; DB 22; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.9e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTRVLQGVLPALPQVVC 17
 Db 1 MTRVLQGVLPALPQVVC 17
 RESULT 2
 AAP91856
 ID AAP91856 standard; peptide; 20 AA.
 XX
 AC AAP91856;
 XX
 DT 07-MAR-1990 (first entry)
 XX
 DE 38-57 region of human chorionic gonadotropin.
 XX
 KW Human chorionic gonadotropin; beta-subunit; analogue; antibodies.
 OS Homo sapiens.
 XX
 PN US4855285-A.
 XX
 PD 08-AUG-1989.
 XX
 CC The peptide is modified outside the body, eg with diphtheria toxoid, then

PF 17-AUG-1987; 87US-0086401.
 XX
 PR 04-DEC-1985; 85US-0804642.
 PR 17-AUG-1987; 87US-0086401.
 XX
 PA (OHIS) OHIO STATE UNIVERSITY RESEARCH FOUNDATION.
 XX
 PI Stevens VC;
 XX
 DR WPI; 1989-285270/39.
 XX
 PT Controlling biological activity of chorionic gonadotropin
 PT - by administering a peptide comprising the 38-57 region coupled to
 PT material to evoke antibodies.
 XX
 PS Disclosure; page 14; 82pp; English.
 XX
 CC The peptide is the 38-57 region of human chorionic gonadotropin.
 CC Peptide is coupled to a target material, eg poly(lysine) or diphtheria
 CC or cholera toxoid, epichlorohydrin, etc, and used to form antibodies in
 CC primates which control chorionic gonadotropin activity. When the carrier
 CC is poly(lysine), a second polypeptide is added to increase antigenicity.
 CC The peptide can be used for contraception, abortion, to treat hormone-
 CC related diseases and disorders, hormone-associated carcinoma and to boost
 CC resistance to exogenous, eg viral, proteins.
 XX
 SQ Sequence 20 AA;
 Query Match 100.0%; Score 86; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.4e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTRVLQGVLPALPQVVC 17
 Db 4 MTRVLQGVLPALPQVVC 20
 RESULT 3
 AAP90568
 ID AAP90568 standard; peptide; 20 AA.
 XX
 AC AAP90568;
 XX
 DT 31-JAN-1990 (first entry)
 XX
 DE Peptide similar to the 38-57 region of beta-subunit of human chorionic
 DE gonadotropin.
 XX
 KW Human chorionic gonadotropin.
 XX
 OS Homo sapiens.
 XX
 PN US4855285-A.
 XX
 PD 08-AUG-1989.
 XX
 PF 17-AUG-1987; 87US-0086401.
 XX
 PR 04-DEC-1985; 85US-0804642.
 XX
 PA (OHIS) OHIO STATE UNIVERSITY.
 XX
 PI Stevens VC;
 XX
 DR WPI; 1989-285270/39.
 XX
 PT Controlling biological activity of chorionic gonadotropin - by
 PT administering a peptide comprising the 38-57 region coupled to material
 PT to evoke antibodies.
 XX
 PS Claim 9; page 57; 82pp; english.
 XX
 CC The peptide is modified outside the body, eg with diphtheria toxoid, then


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RESULT 6
AAB15353
ID AAB15353 standard; peptide; 20 AA.
XX
AC AAB15353;
XX
DT 15-FEB-2001 (first entry)
XX
DE Human chorionic gonadotropin beta-subunit loop peptide.
XX
KW Human; chorionic gonadotropin; hCG; DNA vaccine; cancer;
KW fertility control; contraceptive; immunogen.
XX
OS Homo sapiens.
FH
FT Key Location/Qualifiers
FT Disulfide-bond 1..20
XX
PN WO200041717-A2.
XX
PD 20-JUL-2000.
XX
PF 17-DEC-1999; 99WO-US30232.
XX
PR 18-DEC-1998; 98US-0112910.
XX
PA (AVIB-) AVI BIOPHARMA INC.
XX
PI Iversen PL;
XX
DR WPI; 2000-466124/40.
DR N-PSDB; AAA73831.
XX
PT Inducing immune response to human chorionic gonadotropin (hCG), useful
PT for treatment of cancer and fertility control comprises exposing cells
PT to nucleic acid construct encoding hCG immunogenic epitope -
XX
PS Claim 24; Fig 1H; 45pp; English.
XX
CC The present sequence comprises part of the human chorionic
CC gonadotropin (hCG) beta-subunit, which forms a loop due to the
CC presence of two cysteine residues. It was used in the methods of the
CC invention which involve the use of DNA vaccines encoding hCG antigens
CC to induce an immune response and enable the treatment of cancer and
CC provide a novel method of fertility control. In particular, they can be
CC used to treat colorectal, breast and lung cancer, as hCG is associated
CC with these types of tumours.
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 86; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
   |||||
Db 4 MTRVLQGVLPALPQVVC 20

RESULT 7
AAU02856
ID AAU02856 standard; Peptide; 20 AA.
XX
AC AAU02856;
XX
DT 07-SEP-2001 (first entry)
XX
DE Peptide containing residues 38-57 of betaHCG #3.
XX
KW Human chorionic gonadotropin beta-subunit; hCG; mammal; pregnancy test;
KW human pituitary luteinising hormone; reduced fertility; infertility;
KW contraception; abortion; hormone-associated carcinoma.
XX

Query Match 100.0%; Score 86; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
   |||||
Db 4 MTRVLQGVLPALPQVVC 20

RESULT 8
AAU02871
ID AAU02871 standard; Peptide; 20 AA.
XX
AC AAU02871;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human Chorionic Gonadotropin (HCG) beta-subunit mutated fragment #1.
XX
KW Human chorionic gonadotropin beta-subunit; hCG; mammal; pregnancy test;
KW human pituitary luteinising hormone; reduced fertility; infertility;
KW contraception; abortion; hormone-associated carcinoma.
XX
OS Homo sapiens.
XX
PN WO200124765-A2.
XX
PD 12-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US27741.
XX
PR 06-OCT-1999; 99US-0413564.
XX
PA (OHIS ) UNIV OHIO STATE RES FOUND.
XX
PI Stevens VC;
XX
DR WPI; 2001-328306/34.
XX
PT Peptide analogues of beta-human chorionic gonadotropin which are able to
PT raise antibodies against human chorionic gonadotropin are used in
PT vaccines as contraceptives and/or abortifacients -
XX
PS Disclosure; Page 47; 214pp; English.
XX
CC The sequence represents a peptide containing a fragment of the
CC beta-subunit of human chorionic gonadotropin (betaHCG). Peptide
CC analogues of amino acid residues 38-57 of betaHCG have a disulfide bridge
CC linking the cysteine residues at positions 38 and 57 to form a loop
CC structure. The peptides are used in vaccines to raise antibodies against
CC hCG with a significant decrease in antibodies reactive to human pituitary
CC luteinising hormone, to control the biological activity of endogenous
CC hCG. These antibodies may be used in diagnostic tests to determine
CC hormone levels of mammals. The peptides can be used in pregnancy tests
CC and in detection of reduced fertility or infertility. They may also be
CC administered for contraception or abortion processes. Upon conjugation to
CC a foreign carrier, the peptides may be administered to humans to treat
CC hormone-associated carcinomas.
XX
SQ Sequence 20 AA;

Query Match 100.0%; Score 86; DB 22; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
   |||||
Db 4 MTRVLQGVLPALPQVVC 20

RESULT 8
AAU02871
ID AAU02871 standard; Peptide; 20 AA.
XX
AC AAU02871;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human Chorionic Gonadotropin (HCG) beta-subunit mutated fragment #1.
XX
KW Human chorionic gonadotropin beta-subunit; hCG; mammal; pregnancy test;
KW human pituitary luteinising hormone; reduced fertility; infertility;
KW contraception; abortion; hormone-associated carcinoma.
XX
OS Homo sapiens.
XX
PN WO200124765-A2.
XX
PD 12-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US27741.
XX
PR 06-OCT-1999; 99US-0413564.
XX
PA (OHIS ) UNIV OHIO STATE RES FOUND.
XX
PI Stevens VC;
XX
DR WPI; 2001-328306/34.
XX
PT Peptide analogues of beta-human chorionic gonadotropin which are able to
PT raise antibodies against human chorionic gonadotropin are used in
PT vaccines as contraceptives and/or abortifacients -
XX
PS Disclosure; Page 47; 214pp; English.
XX
CC The sequence represents a peptide containing a fragment of the
CC beta-subunit of human chorionic gonadotropin (betaHCG). Peptide
CC analogues of amino acid residues 38-57 of betaHCG have a disulfide bridge
CC linking the cysteine residues at positions 38 and 57 to form a loop
CC structure. The peptides are used in vaccines to raise antibodies against
CC hCG with a significant decrease in antibodies reactive to human pituitary
CC luteinising hormone, to control the biological activity of endogenous
CC hCG. These antibodies may be used in diagnostic tests to determine
CC hormone levels of mammals. The peptides can be used in pregnancy tests
CC and in detection of reduced fertility or infertility. They may also be
CC administered for contraception or abortion processes. Upon conjugation to
CC a foreign carrier, the peptides may be administered to humans to treat
CC hormone-associated carcinomas.
XX
SQ Sequence 20 AA;

```


PI Stevens VC;
 XX WPI; 2001-328306/34.
 DR
 XX
 PT Peptide analogues of beta-human chorionic gonadotropin which are able to
 PT raise antibodies against human chorionic gonadotropin are used in
 PT vaccines as contraceptives and/or abortifacients -
 XX
 PS Example 43; Page 199; 214pp; English.
 XX
 CC The sequence represents a peptide fragment of the beta-subunit of human
 CC chorionic gonadotropin (betaHCG), mutated for studies on peptides
 CC containing the betaHCG epitope. Peptide analogues of amino acid residues
 CC 38-57 of betaHCG have a disulfide bridge linking the cysteine residues at
 CC positions 38 and 57 to form a loop structure. The peptides are used in
 CC vaccines to raise antibodies against HCG with a significant decrease in
 CC antibodies reactive to human pituitary luteinising hormone, to control
 CC the biological activity of endogenous HCG. These antibodies may be used
 CC in diagnostic tests to determine hormone levels of mammals. The peptides
 CC can be used in pregnancy tests and in detection of reduced fertility or
 CC infertility. They may also be administered for contraception or abortion
 CC processes. Upon conjugation to a foreign carrier, the peptides may be
 CC administered to humans to treat hormone-associated carcinomas.
 XX
 SQ Sequence 20 AA;
 Query Match 100.0%; Score 86; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.4e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTRVLQGVLPALPOVVC 17
 DB 4 MTRVLQGVLPALPOVVC 20
 RESULT 9
 AAU02875
 ID AAU02875 standard; Peptide; 20 AA.
 XX
 AC AAU02875;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human Chorionic Gonadotropin (HCG) beta-subunit fragment #20.
 XX
 KW Human chorionic gonadotropin beta-subunit; HCG; mammal; pregnancy test;
 KW human pituitary luteinising hormone; reduced fertility; infertility;
 KW contraception; abortion; hormone-associated carcinoma.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 2
 FT /label= Hyp
 FT /note= "Hydroxyproline"
 XX
 XX WO200124765-A2.
 XX
 PD 12-APR-2001.
 XX
 XX 06-OCT-2000; 2000WO-US27741.
 PF
 XX
 PR 06-OCT-1999; 99US-0413564.
 XX
 PA (OHIS) UNIV OHIO STATE RES FOUND.
 XX
 PI Stevens VC;
 XX
 XX WPI; 2001-328306/34.
 DR Peptide analogues of beta-human chorionic gonadotropin which are able to
 XX raise antibodies against human chorionic gonadotropin are used in
 PT vaccines as contraceptives and/or abortifacients -
 PT

XX Claim 1; Page 208; 214pp; English.
 PS
 XX
 CC The sequence represents a peptide fragment of the beta-subunit of human
 CC chorionic gonadotropin (betaHCG), mutated for studies on peptides
 CC containing the betaHCG epitope. Peptide analogues of amino acid residues
 CC 38-57 of betaHCG have a disulfide bridge linking the cysteine residues at
 CC positions 38 and 57 to form a loop structure. The peptides are used in
 CC vaccines to raise antibodies against HCG with a significant decrease in
 CC antibodies reactive to human pituitary luteinising hormone, to control
 CC the biological activity of endogenous HCG. These antibodies may be used
 CC in diagnostic tests to determine hormone levels of mammals. The peptides
 CC can be used in pregnancy tests and in detection of reduced fertility or
 CC infertility. They may also be administered for contraception or abortion
 CC processes. Upon conjugation to a foreign carrier, the peptides may be
 CC administered to humans to treat hormone-associated carcinomas.
 XX
 SQ Sequence 20 AA;
 Query Match 100.0%; Score 86; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.4e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTRVLQGVLPALPOVVC 17
 DB 4 MTRVLQGVLPALPOVVC 20
 RESULT 10
 AAU01158
 ID AAU01158 standard; peptide; 20 AA.
 XX
 AC AAU01158;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Structure XXVII (peptide #1), derived from the HCG beta-subunit.
 XX
 KW Human chorionic gonadotropin; HCG; contraception; abortion;
 KW hormone-related disorder; hormone-associated carcinoma; cancer; diabetes;
 KW vascular disease; Zollinger-Ellison syndrome; chronic digestive disorder;
 KW antigenic modification; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..20
 FT /note= "Optionally present to form a cyclised peptide"
 XX
 XX US6217881-B1.
 PN
 XX 17-APR-2001.
 PD
 XX 06-JUN-1995; 95US-0467997.
 PF
 XX 06-OCT-1992; 92US-0958601.
 PR 07-AUG-1992; 92US-0390530.
 PR 04-DEC-1985; 85US-0804642.
 PR 17-AUG-1987; 87US-0086401.
 XX
 PA (OHIS) UNIV OHIO STATE RES FOUND.
 XX
 PI Stevens VC;
 XX
 XX WPI; 2001-289819/30.
 DR
 XX
 PT Novel vaccine composition for provoking the formation of antibodies to
 PT human chorionic gonadotropin, contains a peptide comprising disulfide
 PT bridges linking terminal cysteine residues to form a loop -
 XX
 PS Disclosure; Column 26; 82pp; English.
 XX

CC The present sequence represents Structure XXVII which is analogous to
 CC amino acids 38-57 of the beta-subunit of human chorionic gonadotropin
 CC (HCG). The present peptide is 1 of various structures described
 CC (AAU01140-AAU01174) which can be synthetically modified to make them more
 CC strongly antigenic, thereby provoking the formation of relatively large
 CC quantities of antibodies to the non-endogenous materials in the body of
 CC the animals, with consequent reduced risk of damage to the immune
 CC system, if exposed to non-endogenous materials. The HCG beta-subunit
 CC polypeptide sequence (AAU01139) is used to isolate 3 novel HCG antigenic
 CC peptides (AAU01175-AAU01177) with a disulfide bridge linking the terminal
 CC cysteine amino acids to form a loop, and conjugated to a carrier. The
 CC HCG antigenic peptides can be used in a vaccine composition for
 CC provoking an antibody response to HCG in a mammal. The novel HCG
 CC antigenic peptides are useful for the purpose of contraception,
 CC abortion, and for the treatment of hormone-related disease states and
 CC disorders, treatment of hormone-associated carcinomas, and to boost an
 CC animal's resistance to exogenous proteins, such as viral proteins. The
 CC HCG antigenic peptides are also useful for treating cancer, diabetes,
 CC vascular disease, hypertension, Zollinger-Ellison syndrome, and
 CC chronic digestive disorders.

XX Sequence 20 AA;

Query Match 100.0%; Score 86; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.4e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
 DB 4 MTRVLQGVLPALPQVVC 20
 |||||

RESULT 11

AB49904
 ID AAB49904 standard; protein; 20 AA.

XX AC AAB49904;

DT 06-MAR-2001 (first entry)

DE Human chorionic gonadotropin hCG loop peptide.

KW Human; chorionic gonadotropin; hCG; cancer; vaccine;
 immunogenic epitope.

XX OS Homo sapiens.

XX PN WO200069915-A2.

XX PD 23-NOV-2000.

XX PF 15-MAY-2000; 2000WO-US13392.

XX PR 17-MAY-1999; 99US-0134419.

XX PR 17-MAY-1999; 99US-0134432.

XX PA (AVTB-) AVI BIOPHARMA INC.

XX PI Iversen PL;

XX DR WPI; 2001-025010/03.

XX Human, anti-human chorionic gonadotropin (hCG) monoclonal antibody
 PT immunoreactive with a 21mer N-terminal fragment of C-terminal 37
 PT subunits of hCG beta subunit, used to treat cancer along with vaccine
 PT comprising hCG groups -

XX Claim 10; Fig 2H; 40pp; English.

CC The present invention provides the sequences of several immunogenic
 CC epitopes and antibodies to human chorionic gonadotropin (hCG). These can
 CC be used in the treatment of cancers where hCG synthesis occurs, including
 CC bladder, pancreatic, cervical, colorectal, lung, oesophageal, breast,

CC gastric, prostate, ovarian, uterine and endometrial cancers.
 XX Sequence 20 AA;

Query Match 100.0%; Score 86; DB 22; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3.4e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
 DB 4 MTRVLQGVLPALPQVVC 20
 |||||

RESULT 12

AA71013
 ID AAP71013 standard; protein; 22 AA.

XX AC AAP71013;

XX DT 05-APR-1991 (first entry)

XX DE Sequence of fragment XVII of human chorionic gonadotropin (HCG) beta
 DE subunit.

XX KW Fertility control; vaccine; Zollinger-Ellison syndrome; diabetes;
 XX hypertension.

XX OS Homo sapiens.

XX PN CA12323206-A.

XX PD 23-JUN-1987.

XX PF 16-NOV-1982; 82CA-0415674.

XX PR 04-DEC-1985; 85US-0804462.

XX PR 20-NOV-1981; 81US-0323690.

XX PA (STEV/) STEVENS V C.

XX PI Stevens VC;

XX DR WPI; 1987-199114/29.

XX Vaccines comprising modified polypeptide(s) - have mannide
 PT mono:oleate and squalene or squalene as vehicle for enhanced
 PT efficacy.

XX PS Example; p97; 120pp; English.

XX The vaccines comprise a modified peptide together with, as a
 CC vehicle, a mixt. of mannide mono-oleate with squalene and/or
 CC squalene. The unmodified peptide is typically a fragment of HCG,
 CC eg a specified polypeptide having 37 AAs. The fragment may be
 CC modified by being coupled to diphtheria toxoid, eg at 20-30
 CC fragments per 100,000 daltons of toxoid. Cys residues may be linked
 CC through a disulphide bridge, and AA sequences may be attached
 CC through an AA spacer to a carrier. The vaccines may be used to
 CC treat Zollinger-Ellison syndrome, hypertension, diabetes and
 CC associated micro-and macro-vascular diseases, and endocrine or
 CC hormone dependent breast tumours or cancers. The vaccine may also
 CC be used for fertility control.

XX Sequence 22 AA;

Query Match 100.0%; Score 86; DB 8; Length 22;
 Best Local Similarity 100.0%; Pred. No. 3.8e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
 DB 6 MTRVLQGVLPALPQVVC 22
 |||||

RESULT 13
 AAB64086
 ID AAB64086 standard; peptide; 24 AA.
 AC AAB64086;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Human Clara cell protein-derived antiviral peptide, SEQ ID NO:39.
 XX
 DE Human Clara cell protein-derived peptide; CC10; antiviral;
 KW immune potentiator; anti-infective; therapy; prophylaxis;
 KW Clara cell receptor-independent; inhibin expression inducer.
 KW pro-apoptotic; anticancer; non-immunogenic; retrovirus; togavirus;
 KW flavivirus; rubivirus; pestivirus; hantavirus; HIV; human herpes virus;
 KW hepatitis virus; cytomegalovirus; autoimmune disease;
 KW septic shock syndrome; cachexia; tumour; reverse transcriptase inhibitor;
 KW p24 inhibitor.
 XX
 OS Homo sapiens.
 XX
 PN WO200072868-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 01-JUN-2000; 2000WO-IB00895.
 XX
 PR 01-JUN-1999; 99US-0137227.
 PR 03-MAR-2000; 2000IE-0000170.
 PR 13-APR-2000; 2000IE-0000303.
 PR 18-MAY-2000; 2000IE-0000385.
 PR 18-MAY-2000; 2000IE-0000386.
 XX
 PA (PREN/) PRENDERGAST P T.
 XX
 PI Prendergast PT;
 XX
 DR WPI; 2001-146767/15.
 XX
 PT Novel pharmaceutical formulation comprising a compound that comprises a
 PT peptide isolated from Clara cell protein useful for treating autoimmune
 PT disorders, cancers, viral infections, septic shock syndrome and
 PT cachexia -
 XX
 PS Claim 1; Page 92-93; 139pp; English.
 XX
 CC The invention relates to pharmaceutical compositions comprising
 CC therapeutic peptides corresponding to human Clara cell protein
 CC fragments or conservative variants thereof (AAB64050-B64178). The
 CC peptides of the invention, unlike native Clara cell protein, have
 CC potent antiviral activity, being able to block viral replication via
 CC the inhibition of reverse transcriptase and p24 activities. The
 CC Clara cell-derived proteins of the invention also have a broad immune
 CC potentiator effect and anti-infective (antibacterial and antifungal, as
 CC well as antiviral) activity. The peptides of the invention may also
 CC induce the synthesis of inhibin, a secreted protein with tumour
 CC suppressor activity, and may also upregulate the expression of
 CC pro-apoptotic genes. The peptides may additionally mimic the effects of
 CC full-term pregnancy with respect to long-term protection against
 CC chemical carcinogens and lifetime reduction in breast cancer risk,
 CC and also inhibit prostaglandin-induced pre-term delivery. The
 CC peptides induce functional maturation of cortical thymocytes, and act as
 CC a factor regulating antigen-independent differentiation of T-lymphocytes
 CC during pregnancy, thus enhancing the immune system in embryogenesis.
 CC The peptides of the invention are non-immunogenic, and function without
 CC the requirement for Clara cell receptors. The peptides are used
 CC prophylactically and therapeutically against viral infections,
 CC specifically infections caused by retroviruses, togaviruses,
 CC flaviviruses, rubiviruses, pestiviruses and hantaviruses, and
 CC particularly infections by HIV, human T-lymphocyte virus 1 (HTLV-1),
 CC HTLV-3, Kaposi's Sarcoma-associated herpes virus, human herpes virus 6
 CC (HHV-6), HHV-8, viruses of the genus Molluscipoxvirus, hepatitis A, B,
 CC

or C virus, or cytomegalovirus. The peptides can also be used to reduce
 the likelihood of septic shock syndrome in a patient about to undergo
 surgery, and can be used to treat this condition in a post-operative
 patient. They can also reduce the likelihood of cachexia in a patient
 about to undergo surgery. The peptides can be used to treat autoimmune
 conditions such as multiple sclerosis, systemic lupus erythematosus,
 myasthenia gravis, rheumatoid arthritis, Sjogren's disease, ulcerative
 colitis, and diabetes or to ameliorate immune damage and/or disease
 progression. The peptides can also be used to treat cancer, or to slow
 progression or development of cancers such as breast cancer, colon
 cancer, leukaemia, brain cancer, lung cancer and melanoma. The
 present sequence represents a human Clara cell protein-derived peptide
 of the invention.
 SQ Sequence 24 AA;
 Query Match 100.0%; Score 86; DB 22; Length 24;
 Best Local Similarity 100.0%; Pred. No. 4.2e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTRVLQGVLPALPQVVC 17
 DQ 6 MTRVLQGVLPALPQVVC 22
 RESULT 14
 AAB64108
 ID AAB64108 standard; peptide; 25 AA.
 AC AAB64108;
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE Human Clara cell protein-derived antiviral peptide, SEQ ID NO:61.
 XX
 DE Human Clara cell protein-derived peptide; CC10; antiviral;
 KW immune potentiator; anti-infective; therapy; prophylaxis;
 KW Clara cell receptor-independent; inhibin expression inducer.
 KW pro-apoptotic; anticancer; non-immunogenic; retrovirus; togavirus;
 KW flavivirus; rubivirus; pestivirus; hantavirus; HIV; human herpes virus;
 KW hepatitis virus; cytomegalovirus; autoimmune disease;
 KW septic shock syndrome; cachexia; tumour; reverse transcriptase inhibitor;
 KW p24 inhibitor.
 XX
 OS Homo sapiens.
 XX
 PN WO200072868-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 01-JUN-2000; 2000WO-IB00895.
 XX
 PR 01-JUN-1999; 99US-0137227.
 PR 03-MAR-2000; 2000IE-0000170.
 PR 13-APR-2000; 2000IE-0000303.
 PR 18-MAY-2000; 2000IE-0000385.
 PR 18-MAY-2000; 2000IE-0000386.
 XX
 PA (PREN/) PRENDERGAST P T.
 XX
 PI Prendergast PT;
 XX
 DR WPI; 2001-146767/15.
 XX
 PT Novel pharmaceutical formulation comprising a compound that comprises a
 PT peptide isolated from Clara cell protein useful for treating autoimmune
 PT disorders, cancers, viral infections, septic shock syndrome and
 PT cachexia -
 XX
 PS Claim 1; Page 103; 139pp; English.
 XX
 CC The invention relates to pharmaceutical compositions comprising
 CC therapeutic peptides corresponding to human Clara cell protein

CC fragments or conservative variants thereof (AAB64050-B64178). The
 CC peptides of the invention, unlike native Clara cell protein, have
 CC potent antiviral activity, being able to block viral replication via
 CC the inhibition of reverse transcriptase and p24 activities. The
 CC Clara cell-derived proteins of the invention also have a broad immune
 CC potentiator effect and anti-infective (antibacterial and antifungal, as
 CC well as antiviral) activity. The peptides of the invention may also
 CC induce the synthesis of inhibin, a secreted protein with tumour
 CC suppressor activity, and may also upregulate the expression of
 CC pro-apoptotic genes. The peptides may additionally mimic the effects of
 CC full-term pregnancy with respect to long-term protection against
 CC chemical carcinogens and lifetime reduction in breast cancer risk,
 CC and also inhibit prostaglandin-induced pre-term delivery. The
 CC peptides induce functional maturation of cortical thymocytes, and act as
 CC a factor regulating antigen-independent differentiation of T-lymphocytes
 CC during pregnancy, thus enhancing the immune system in embryogenesis.
 CC The peptides of the invention are non-immunogenic, and function without
 CC the requirement for Clara cell receptors. The peptides are used
 CC prophylactically and therapeutically against viral infections,
 CC specifically infections caused by retroviruses, togaviruses,
 CC flaviviruses, rubiviruses, pestiviruses and hantaviruses, and
 CC particularly infections by HIV, human T-lymphocyte virus 1 (HTLV-1),
 CC HTLV-3, Kaposi's Sarcoma-associated herpes virus, human herpes virus 6
 CC (HHV-6), HHV-8, viruses of the genus Molluscipoxvirus, hepatitis A, B,
 CC or C virus, or cytomegalovirus. The peptides can also be used to reduce
 CC the likelihood of septic shock syndrome in a patient about to undergo
 CC surgery, and can be used to treat this condition in a post-operative
 CC patient. They can also reduce the likelihood of cachexia in a patient
 CC about to undergo surgery. The peptides can be used to treat autoimmune
 CC conditions such as multiple sclerosis, systemic lupus erythematosus,
 CC myoscleritis, rheumatoid arthritis, Sjogren's disease, ulcerative
 CC colitis, and diabetes or to ameliorate immune damage and/or disease
 CC progression. The peptides can also be used to treat cancer, or to slow
 CC progression or development of cancers such as breast cancer, colon
 CC cancer, leukaemia, brain cancer, lung cancer and melanoma. The
 CC present sequence represents a human Clara cell protein-derived peptide
 CC of the invention.

XX Sequence 25 AA;

Query Match 100.0%; Score 86; DB 22; Length 25;
 Best Local Similarity 100.0%; Pred. No. 4.3e-07; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 0;

QY 1 MTRVLQGLPALPQVVC 17

Db 7 MTRVLQGLPALPQVVC 23

RESULT 15

AAU01181

ID AAU01181 standard; peptide; 27 AA.

XX AC AAU01181;

XX AC AAU01181;

XX AC AAU01181;

XX AC AAU01181;

XX AC AAU01181;

XX AC AAU01181;

XX AC AAU01181;

XX AC AAU01181;

XX AC AAU01181;

XX AC AAU01181;

XX AC AAU01181;

XX AC AAU01181;

XX AC AAU01181;

FT Region /note= "Forms a cyclised peptide"
 FT 8..27

FT /note= "Corresponds to native HCG (AAU01139) amino
 FT acids 38-57"

XX US6217881-B1.

XX 17-APR-2001.

XX 06-JUN-1995; 95US-0467997.

XX 06-OCT-1992; 92US-0958601.

XX 07-AUG-1992; 92US-0390530.

XX 04-DEC-1985; 85US-0804642.

XX 17-AUG-1987; 87US-0086401.

XX (OHIS) UNIV OHIO STATE RES FOUND.

XX Stevens VC;

XX WPI; 2001-289819/30.

XX Novel vaccine composition for provoking the formation of antibodies to
 XX human chorionic gonadotropin, contains a peptide comprising disulfide
 XX bridges linking terminal cysteine residues to form a loop -

XX Example 43; Page -; 82pp; English.

XX The present sequence represents human chorionic gonadotropin (HCG)
 XX peptide #1 (Structure XXVII) with a spacer group which can link the
 XX peptide to a carrier such as diphtheria toxoid. The HCG beta-subunit
 XX polypeptide sequence is used to isolate 3 novel HCG antigenic
 XX peptides (AAU01175-AAU01177) with a disulfide bridge linking the
 XX terminal cysteine amino acids to form a loop, and conjugated to a
 XX carrier. The HCG peptides can be used in a vaccine composition for
 XX provoking an antibody response to HCG in a mammal. The novel HCG
 XX antigenic peptides are useful for the purpose of contraception,
 XX abortion, and for the treatment of hormone-associated disease states and
 XX disorders, treatment of hormone-associated carcinomas, and to boost an
 XX animal's resistance to exogenous proteins, such as viral proteins. The
 XX HCG antigenic peptides are also useful for treating cancer, diabetes,
 XX vascular disease, hypertension, Zollinger-Ellison syndrome, and
 XX chronic digestive disorders. Also described are various structures
 XX (AAU01140-AAU01174) which are non-antigenic, non-endogenous materials
 XX which can be synthetically modified to make them more strongly antigenic,
 XX thereby provoking the formation of relatively large quantities of
 XX antibodies to the non-endogenous materials in the body of the animals,
 XX with consequent reduced risk of damage to the immune system, if exposed
 XX to non-endogenous materials.

XX Note: The present sequence is not given in the patent but is indexed
 XX from the information given by the inventor.

XX Sequence 27 AA;

Query Match 100.0%; Score 86; DB 22; Length 27;

Best Local Similarity 100.0%; Pred. No. 4.7e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGLPALPQVVC 17

Db 11 MTRVLQGLPALPQVVC 27

RESULT 16

AAP91836

ID AAP91836 standard; peptide; 60 AA.

XX AC AAP91836;

XX AC AAP91836;

XX AC AAP91836;

XX AC AAP91836;

XX AC AAP91836;

XX AC AAP91836;

KW Human chorionic gonadotropin; beta-subunit; antibodies;
 KW disulphide bridge.

XX Homo sapiens.

XX US4855285-A.

XX 08-AUG-1989.

XX 17-AUG-1987; 87US-0086401.

XX 04-DEC-1985; 85US-0804642.

XX 17-AUG-1987; 87US-0086401.

XX (OHIS) OHIO STATE UNIVERSITY RESEARCH FOUNDATION.

XX Stevens VC;

XX WPI; 1989-285270/39.

XX Controlling biological activity of chorionic gonadotropin
 PT - by administering a peptide comprising the 38-57 region coupled to
 PT material to evoke antibodies.

XX Disclosure; page 10; 82pp; English.

XX The peptide is coupled to a target material, eg poly(lysine), diphtheria
 CC or cholera toxoid, epichlorohydrin, etc, and used to form antibodies in
 CC primates which control chorionic gonadotropin activity. The peptide has
 CC a high degree of structural homology with corresp. luteinising hormone
 CC subunit. When the carrier is poly(lysine), a second polypeptide is added
 CC to increase antigenicity. The unmodified peptide may have a spacer
 CC sequence attached at residue 38, which has an N-terminal residue involved
 CC in coupling. The peptide can be used for contraception, abortion, to
 CC treat hormone-related disorders, hormone-associated carcinoma
 CC and to boost resistance to exogenous, eg viral, proteins.

XX Sequence 60 AA;

Query Match 100.0%; Score 86; DB 10; Length 60;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17

DB 41 MTRVLQGVLPALPQVVC 57

RESULT 17

AAW95536
 ID AAW95536 standard; protein; 85 AA.

XX AAW95536;

XX 24-MAR-1999 (first entry)

XX Human chorionic gonadotropin (hCG) beta subunit analogue.

XX Human; chorionic gonadotropin; hCG; three-dimensional; 3D; analogue;
 KW molecular simulation; visual display; chemical structure; growth factor;
 KW N-glycosylation site; follicle stimulating hormone; luteinising hormone;
 KW thyroid stimulating hormone; in vitro fertilisation; fertility; mutation;
 KW beta subunit; glycoprotein.

XX Homo sapiens.

XX Synthetic.

XX Key Location/Qualifiers

XX Modified-site 60...62

XX /note= "Asn is N-glycosylated; see claim 4"

XX US5864488-A.

XX

PD 26-JAN-1999.

XX 24-FEB-1995; 95US-0395238.

XX 24-FEB-1994; 94GB-0003600.

XX (UNIU) UNIV GLASGOW.

XX Grootenhuis PDJ, Harris DC, Isaacs NW, Laphorn AJ;

XX WPI; 1999-131522/11.

XX Determining the 3-dimensional coordinates of chorionic gonadotropin
 PT and computer-assisted re-design of the chemical structure - used for
 PT production of gonadotropin hormone analogues

XX Disclosure; Page -: 60pp; English.

XX The invention relates to determining whether an analogue of human
 CC chorionic gonadotropin (hCG) will have an altered three-dimensional (3D)
 CC structure as compared to hCG. Analogues of hCG and other glycoprotein
 CC hormones are produced by inputting chemical changes to the 3D structure
 CC into a computer loaded with 3D molecular simulation software and
 CC representing visually on a computer display. On inputting into the data
 CC input of the computer at least one operator change in chemical structure
 CC of the hCG molecule, the molecular simulation software produces a
 CC modified 3D molecular representation of the analogue structure. The 3D
 CC representation of the analogue can be displayed on the visual display,
 CC whereby changes in 3D structure of the hCG molecule consequent on changes
 CC in chemical structure can be visually determined. Glycoprotein analogues
 CC with additional glycosylation sites, and analogues with non-essential
 CC hairpins deleted can be produced by this method. The methods can be used
 CC to obtain analogues of hCG, follicle stimulating hormone, luteinising
 CC hormone, thyroid stimulating hormone, which may act as agonists or
 CC antagonists. The analogues can be used as growth factors in mammals, for
 CC in vitro fertilisation techniques and for treatment in vivo to enhance
 CC fertility. The present sequence represents an analogue of the beta
 CC subunit of hCG. The changes in the chemical structure inputted into the
 CC data resulted in the deletion of a hairpin loop in the beta subunit
 CC (residues 60-85) to produce a structure .beta(1-59)D-S-N.beta(86-108).
 CC Note: this sequence is not provided in the specification; it has been
 CC created by modifying the hCG beta subunit sequence in Fig 2 and
 CC utilising the structure given in claim 4.

XX Sequence 85 AA;

Query Match 100.0%; Score 86; DB 20; Length 85;

Best Local Similarity 100.0%; Pred. No. 1.5e-06;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17

DB 41 MTRVLQGVLPALPQVVC 57

RESULT 18

AAU04621

ID AAU04621 standard; protein; 93 AA.

XX AAU04621;

XX 23-OCT-2001 (first entry)

XX Human chorionic gonadotropin (hCG) beta, amino acids 1-93.

XX Human; chorionic gonadotropin; hCG; glycoprotein hormone; infertility;
 KW luteinising hormone; LH; follicle stimulating hormone; FSH;
 KW thyroid stimulating hormone; TH.

XX Homo sapiens.

XX US6242580-B1.

XX

PD 05-JUN-2001.
 XX 31-MAR-1999; 99US-0282357.
 PF 25-AUG-1997; 97US-0918288.
 XX 18-FEB-1994; 94US-0199382.
 PR 12-AUG-1994; 94US-0289396.
 PR 22-SEP-1994; 94US-0310590.
 PR 04-NOV-1994; 94US-0334628.
 PR 07-DEC-1994; 94US-0351591.
 PR 07-JUN-1995; 95US-0475049.
 PR 09-MAY-1997; 97US-0853524.
 XX (UNIW) UNIV WASHINGTON.
 PA Boime I, Moyle WR;
 XX WPI; 2001-424301/45.
 DR New single chain forms of the glycoprotein hormone quartet useful for
 XX generating antibodies specifically immunoreactive with the new
 PT compounds, in treating infertility, or as aids for in vivo
 PT fertilization techniques -
 XX Example 19; Column 34-35; 86pp; English.
 PS The sequence represents the amino acid sequence of human chorionic
 CC gonadotropin (hCG) beta, amino acids 1-93. The protein is an
 CC important glycoprotein hormone heterodimer, along with luteinizing
 CC hormone (LH), follicle stimulating hormone (FSH), thyroid stimulating
 CC hormone (TH), which all have identical alpha subunits but differing beta
 CC subunits. The proteins are useful for generating antibodies specifically
 CC immunoreactive with new compounds, as substitutes for the
 CC heterodimeric forms of the hormones, in the treatment of infertility, as
 CC aids for in vivo fertilisation techniques, and in other therapeutic
 CC methods associated with the native hormones. The single chain proteins
 CC are further useful as reagents in a manner similar to the heterodimers,
 CC as diagnostic tools to detect the presence of antibodies with respect to
 CC the native proteins in the biological samples, as control reagents in
 CC assay kits for assessing the levels of these hormones in various samples,
 CC and in detecting and purifying receptors to which the native hormones
 CC bind. The single chain forms of the heterodimers or homodimers have the
 CC following advantages over their dimeric forms: they are more stable,
 CC problems of recombinant production are reduced since only a single gene
 CC is needed to transcribe, translate and process, provide an alternate form
 CC thus permitting fine tuning of activity levels and of in vivo half lives.
 CC Single chain forms are unique starting materials for identifying
 CC truncated forms with the activity of the dimer. The linkage between the
 CC subunits permits the protein to be engineered without disturbing the
 CC overall folding of the protein.
 XX Sequence 93 AA;
 SQ Query Match 100.0%; Score 86; DB 22; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTRVLQGVLPALPQVVC 17
 DB 41 MTRVLQGVLPALPQVVC 57
 |||||
 RESULT 19
 AAE04493
 ID AAE04493 standard; Protein; 93 AA.
 XX AAE04493;
 AC
 XX
 DT 04-SEP-2001 (first entry)
 XX Human chorionic gonadotropin beta-subunit fragment (1-93 amino acids).
 DE Human; single chain gonadotropin analog; anti-infertility; drug;
 XX
 KW peptide therapy; luteinising hormone; LH; follicle stimulating hormone;
 KW FSH; thyroid stimulating hormone; TSH; chorionic gonadotropin; CG;
 KW glycoprotein; infertility; fusion protein.
 XX Homo sapiens.
 XX US6238890-B1.
 XX 29-MAY-2001.
 XX 25-AUG-1997; 97US-0918288.
 PF 18-FEB-1994; 94US-0199382.
 XX 12-AUG-1994; 94US-0289396.
 PR 22-SEP-1994; 94US-0310590.
 PR 04-NOV-1994; 94US-0334628.
 PR 07-DEC-1994; 94US-0351591.
 PR 07-JUN-1995; 95US-0475049.
 PR 09-MAY-1997; 97US-0853524.
 XX (UNIW) UNIV WASHINGTON.
 PA Boime I, Moyle WR;
 XX WPI; 2001-366474/38.
 DR New DNA or RNA encoding single chain protein useful in treating
 XX infertility, as aids in vitro fertilization techniques, or other
 PT therapeutic methods associated with the native hormones -
 XX Example 19; Column 33; 87pp; English.
 PS The invention relates to human single chain forms of the glycoprotein
 CC hormone quartet which is an agonist or antagonist of luteinising hormone
 CC (LH), follicle stimulating hormone (FSH), thyroid stimulating hormone
 CC (TSH) or chorionic gonadotropin (CG). All these hormones are heterodimers
 CC having identical alpha subunits and differing beta subunits. The agonist
 CC forms of single chain hormones are used in treating infertility, as aids
 CC in vitro fertilisation techniques, and other therapeutic methods
 CC associated with the native hormones. The single chain hormones are useful
 CC as reagents in a manner similar to heterodimers, as diagnostic tools to
 CC detect the presence of antibodies with respect to the native proteins in
 CC biological samples, as control reagents in assay kits for assessing the
 CC levels of these hormones in various samples, in detecting and purifying
 CC receptors to which the native hormones bind. The single chain hormones
 CC are also used in affinity chromatographic preparation of receptors or
 CC antihormone antibodies. They are used as purification tools for
 CC isolation of subsequent preparations of these materials and to monitor
 CC levels of single chain hormones administered as drugs. The single chain
 CC glycoproteins are used to generate antibodies specifically immunoreactive
 CC with these new compounds, as substitutes for the heterodimeric forms of
 CC hormones. The present sequence is human chorionic gonadotropin beta-
 CC subunit fragment (1-93 amino acids) which is used for constructing
 CC single chain gonadotropin analogs related to the invention. Analog
 CC fusion proteins serves as useful starting compounds for template directed
 CC vaccine design and for the development of hormone-specific vaccines for
 CC use in humans.
 XX Sequence 93 AA;
 SQ Query Match 100.0%; Score 86; DB 22; Length 93;
 Best Local Similarity 100.0%; Pred. No. 1.7e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTRVLQGVLPALPQVVC 17
 DB 41 MTRVLQGVLPALPQVVC 57
 |||||
 RESULT 20
 AAR15161
 ID AAR15161 standard; Protein; 111 AA.
 XX

AC AAR15161;
 XX 11-FEB-1992 (first entry)
 DT
 DE hCG deletion mutant, F1.
 XX
 KW Glycoprotein hormone; immuno-castration;
 XX immuno-contragestive; vaccine; human chorionic gonadotropin;
 OS Homo sapiens.
 XX
 PN WO9116922-A.
 XX
 PD 14-NOV-1991.
 XX
 PF 07-MAY-1991; 91WO-US03162.
 XX
 PR 08-MAY-1990; 90US-0520703.
 XX
 PA (UYNE-) UNIV MED NEW JERSEY.
 XX
 PI Campbell RK, Moyle WR;
 XX
 DR WPI; 1991-353528/48.
 XX
 XX New glyco-protein hormone analogues - for inducing fertility as
 PT immuno-castration agents, for suppressing reproductive system
 PT development and as immuno-contragestive vaccines.
 XX
 XX Table VII; Page 66; 94pp; English.
 XX
 CC The sequence is an analogue of mature hCG beta subunit having
 CC residues 112-145 deleted. It was prepd. using PCR mutagenesis to
 CC insert a stop codon into the gene. It may be useful as an agonist
 CC for suppression of gonadal activity during chemotherapy.
 CC See AAR15043, AAR15061-R15125 and AAR15162-R15198.
 XX
 XX Sequence 111 AA;
 SQ
 Query Match 100.0%; Score 86; DB 12; Length 111;
 Best Local Similarity 100.0%; Pred. No. 2e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTRVLQGVLPALPQVVC 17
 DB 41 MTRVLQGVLPALPQVVC 57
 RESULT 21
 AAR31003
 ID AAR31003 standard; protein; 114 AA.
 XX
 AC AAR31003;
 XX
 DT 14-MAY-1993 (first entry)
 XX
 DE Modified hCG beta-subunit - analogue "g".
 XX
 KW hCG; glycoprotein hormone analogue; human infertility; LH; FSH;
 KW luteinising hormone receptor; follicle stimulating hormone receptor;
 KW vertebrate; polycystic ovarian disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 101..109
 FT /note= "non-hCG derived residues"
 FT Region 94..97
 FT /note= "D region - LH binding and specificity"
 FT Region 100..106
 FT /note= "G region - FSH binding and specificity"
 XX
 PN WO9222568-A.

XX 23-DEC-1992.
 PD
 XX 18-JUN-1992; 92WO-US05207.
 XX
 PF 18-JUN-1991; 91US-0717151.
 PR
 XX (UYNE-) UNIV NEW JERSEY.
 PA
 XX Campbell RK, Moyle WR;
 XX
 PI WPI; 1993-018070/02.
 DR
 XX
 PT New alpha, beta-heterodimeric polypeptide derivs. - which bind to
 PT luteinising and follicle stimulating hormone receptors, useful for
 PT controlling the ratio of FSH to LH activity
 XX
 PS Disclosure; Page 20; 98pp; English.
 XX
 CC The sequence is that of a modified form of human chorionic gonadotrophin
 CC (hCG), analogue "G", in which amino acids in the "D" and/or "G" regions
 CC have been substituted resulting in changes in the binding specificity
 CC and avidity of luteinising hormone (LH) and follicle stimulating
 CC hormone (FSH) receptor. It is used in the prepn. of an alpha,
 CC beta-heterodimeric polypeptide having an affinity to vertebrate LH
 CC and FSH receptors. Such an analogue can be prepared having a desired
 CC ratio of FSH:LH activity. The polypeptide may be used for treating
 CC human infertility or polycystic ovarian disease.
 XX
 XX Sequence 114 AA;
 SQ
 Query Match 100.0%; Score 86; DB 14; Length 114;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTRVLQGVLPALPQVVC 17
 DB 41 MTRVLQGVLPALPQVVC 57
 RESULT 22
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 ID AAR31005 standard; protein; 114 AA.
 XX
 AC AAR31005;
 XX
 DT 14-MAY-1993 (first entry)
 XX
 DE Modified hCG beta-subunit - analogue "Q".
 XX
 KW hCG; glycoprotein hormone analogue; human infertility; LH; FSH;
 KW luteinising hormone receptor; follicle stimulating hormone receptor;
 KW vertebrate; polycystic ovarian disease.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 94..97 "non-hCG derived residues"
 FT /note= "non-hCG derived residues"
 FT Region 94..97
 FT /note= "D region - LH binding and specificity"
 FT Region 100..106
 FT /note= "G region - FSH binding and specificity"
 XX
 PN WO9222568-A.
 XX
 PD 23-DEC-1992.
 XX
 PF 18-JUN-1992; 92WO-US05207.
 XX
 PR 18-JUN-1991; 91US-0717151.
 XX

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XX PA (UYNE-) UNIV NEW JERSEY.
XX PI Campbell RK, Moyle WR;
XX XX WPI; 1993-018070/02.
XX DR
XX XX
XX PT New alpha, beta-hetero:dimeric polypeptide derivs. - which bind to
XX PT luteinising and follicle stimulating hormone receptors, useful for
XX PT controlling the ratio of FSH to LH activity
XX XX
XX PS Disclosure; Page 21; 98pp; English.
XX CC
XX CC The sequence is that of a modified form of human chorionic gonadotrophin
XX CC (hCG), analogue "Q", in which amino acids in the "D" and/or "G" regions
XX CC have been substituted resulting in changes in the binding specificity
XX CC and avidity of luteinising hormone (LH) and follicle stimulating
XX CC hormone (FSH) receptor. It is used in the prepn. of an alpha,
XX CC beta-heterodimeric polypeptide having an affinity to vertebrate LH
XX CC and FSH receptors. Such an analogue can be prepared having a desired
XX CC ratio of FSH:LH activity. The polypeptide may be used for treating
XX CC human infertility or polycystic ovarian disease.
XX XX
XX SQ Sequence 114 AA;

Query Match 100.0%; Score 86; DB 14; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
DB 41 MTRVLQGVLPALPQVVC 57

RESULT 23
ID AAR88920 standard; protein; 114 AA.
XX AC AAR88920;
XX DT 12-JUL-1996 (first entry)
XX DE HCG analogue-G beta-subunit.
XX KW HCG; human; chorionic gonadotropin; beta-subunit; heterodimer;
XX KW alpha-subunit; LH receptor; FSH receptor; LH; FSH; thyrotropin;
XX KW D-region; G-region; protein engineering; fertility; hormone;
XX KW follicle stimulating hormone; luteinising hormone; TSH;
XX KW ovulation; spermatogenesis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Region 1..100
XX FT /note= "HCG sequence"
XX FT Region 94..100
XX FT /note= "HCG D-region"
XX FT Peptide 95..114
XX FT /note= "Fragment encoded by oligonucleotide AAT12942"
XX FT Region 101..109
XX FT /note= "Human FSH G-region"
XX FT Region 110..114
XX FT /note= "HCG sequence"
XX XX
XX PN US5508261-A.
XX PD 16-APR-1996.
XX XX
XX PF 18-JUN-1991; 91US-0717151.
XX PR 21-JAN-1994; 94US-0184408.
XX PR 18-JUN-1991; 91US-0717151.
XX PR 18-AUG-1993; 93US-0108845.

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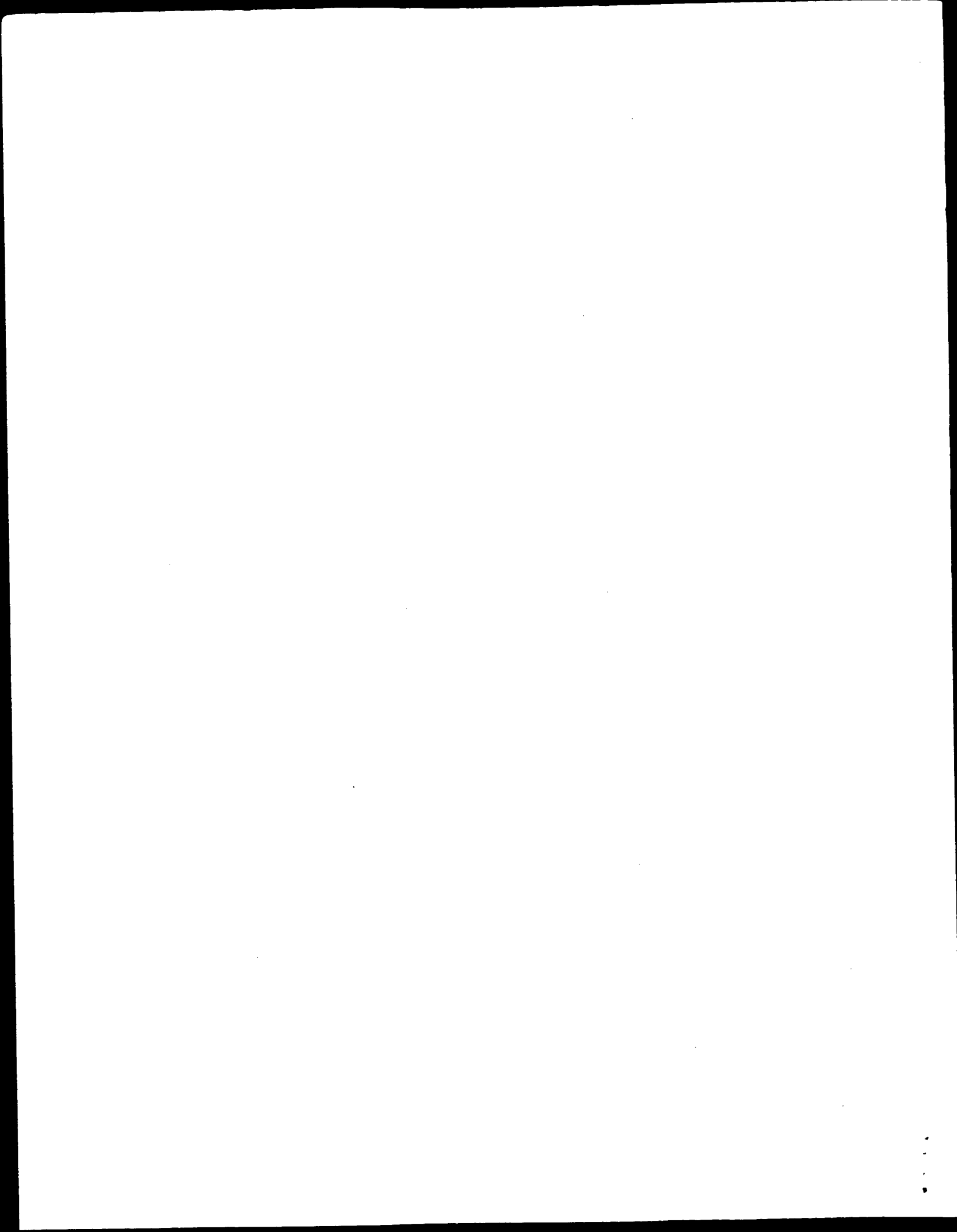
PR 18-APR-1995; 95US-0425673.
XX XX (UYNE-) UNIV NEW JERSEY.
XX PA Campbell RK, Han Y, Macdonald GJ, Moyle WR, Wang Y;
XX PI WPI; 1996-208744/21.
XX DR
XX XX
XX PT New alpha, beta-hetero:dimeric glycoprotein hormone polypeptide(s)
XX PT - having a non-naturally occurring beta-subunit derived from hCG,
XX PT LH, FSH and TSH
XX XX
XX PS Example 1; Column 11-12; 27pp; English.
XX CC
XX CC The sequence is an example of a glycoprotein hormone beta-chain
XX CC analogue used to construct an alpha,beta-heterodimer polypeptide
XX CC with altered binding affinity to LH receptor and FSH receptor. The
XX CC heterodimer preferably contains an HCG alpha-subunit and a chimeric
XX CC beta-subunit containing HCG, LH, FSH and/or thyrotropin residues.
XX CC Binding activity and specificity may be altered without disrupting
XX CC heterodimer formation or reaction with antibodies. The D-region of
XX CC HCG is most important for LH receptor binding, and the G-region is
XX CC and an FSH G-region, has high affinity to both LH and FSH
XX CC receptors. A cDNA for analogue-GT (AAR88924) is digested with BglII
XX CC and SstI and ligated with oligonucleotide AAT12942, followed by
XX CC expression in Escherichia coli DH5-alpha and a COS-7 cell culture.
XX CC An analogue with a low ratio of LH/FSH activity should be useful
XX CC clinically for induction of ovulation in women with polycystic
XX CC ovary disease, or to increase spermatogenesis in azospermic males
XX CC who have some circulating LH.
XX XX
XX SQ Sequence 114 AA;

Query Match 100.0%; Score 86; DB 17; Length 114;
Best Local Similarity 100.0%; Pred. No. 2.1e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
DB 41 MTRVLQGVLPALPQVVC 57

RESULT 24
AAR88921
ID AAR88921 standard; protein; 114 AA.
XX AC AAR88921;
XX DT 13-JUL-1996 (first entry)
XX DE HCG analogue-DG' beta-subunit.
XX KW HCG; human; chorionic gonadotropin; beta-subunit; heterodimer;
XX KW alpha-subunit; LH receptor; FSH receptor; LH; FSH; thyrotropin;
XX KW D-region; G-region; protein engineering; fertility; hormone;
XX KW follicle stimulating hormone; luteinising hormone; TSH;
XX KW ovulation; spermatogenesis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Region 1..93
XX FT /note= "HCG sequence"
XX FT Region 94..114
XX FT /note= "Human FSH D- and G-region"
XX XX
XX PN US5508261-A.
XX PD 16-APR-1996.
XX XX
XX PF 18-JUN-1991; 91US-0717151.
XX XX

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:24:35 ; Search time 14.45 Seconds
(without alignments)
34.615 Million cell updates/sec

Title: US-09-821-380-1

Perfect score: 86

Sequence: 1 MTRVLQGVLPALPQVVC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 65 summaries

Database :

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2: /cgn2.6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2.6/ptodata/1/1aa/6A_COMB.pep: *
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6: /cgn2.6/ptodata/1/1aa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	86	100.0	93	4	US-08-918-288-70
2	86	100.0	93	4	US-09-282-357-70
3	86	100.0	114	1	US-08-425-673-7
4	86	100.0	114	1	US-08-425-673-8
5	86	100.0	114	1	US-08-425-673-9
6	86	100.0	114	4	US-08-918-288-69
7	86	100.0	114	4	US-09-282-357-69
8	86	100.0	117	1	US-08-425-673-11
9	86	100.0	117	1	US-08-425-673-12
10	86	100.0	145	1	US-08-425-673-1
11	86	100.0	145	1	US-08-425-673-2
12	86	100.0	145	1	US-08-425-673-10
13	86	100.0	145	1	US-08-298-189B-1
14	86	100.0	145	1	US-08-475-213-10
15	86	100.0	145	2	US-08-395-238-2
16	86	100.0	145	4	US-09-142-320-4
17	86	100.0	145	4	US-09-142-320-11
18	86	100.0	145	4	US-09-142-320-12
19	86	100.0	145	4	US-09-142-320-13
20	86	100.0	145	4	US-09-142-320-14
21	86	100.0	145	4	US-09-142-320-15
22	86	100.0	145	4	US-09-142-320-16
23	86	100.0	145	4	US-08-918-288-68
24	86	100.0	145	4	US-09-282-357-68
25	86	100.0	145	4	US-08-908-371B-1
26	86	100.0	165	2	US-08-709-924-2
27	86	100.0	165	2	US-08-709-925-2

28	86	100.0	165	4	US-08-709-948-2	Sequence 2, Appli
29	86	100.0	181	4	US-08-918-288-36	Sequence 36, Appl
30	86	100.0	181	4	US-09-282-357-36	Sequence 36, Appl
31	86	100.0	234	4	US-08-918-288-6	Sequence 6, Appli
32	86	100.0	234	4	US-08-918-288-21	Sequence 21, Appl
33	86	100.0	234	4	US-08-918-288-24	Sequence 24, Appl
34	86	100.0	234	4	US-09-282-357-6	Sequence 6, Appli
35	86	100.0	234	4	US-09-282-357-21	Sequence 21, Appl
36	86	100.0	234	4	US-09-282-357-24	Sequence 24, Appl
37	86	100.0	237	4	US-08-918-288-15	Sequence 15, Appl
38	86	100.0	237	4	US-08-918-288-18	Sequence 18, Appl
39	86	100.0	237	4	US-09-282-357-15	Sequence 15, Appl
40	86	100.0	237	4	US-09-282-357-18	Sequence 18, Appl
41	86	100.0	265	4	US-08-918-288-3	Sequence 3, Appli
42	86	100.0	265	4	US-08-918-288-39	Sequence 39, Appl
43	86	100.0	265	4	US-09-282-357-3	Sequence 3, Appli
44	86	100.0	265	4	US-09-282-357-39	Sequence 39, Appl
45	86	100.0	307	4	US-08-804-166-4	Sequence 4, Appli
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47	86	100.0	336	4	US-08-804-166-8	Sequence 8, Appli
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49	71	82.6	14	2	US-08-709-924-12	Sequence 12, Appl
50	71	82.6	14	2	US-08-709-925-12	Sequence 12, Appl
51	71	82.6	14	4	US-08-709-948-12	Sequence 12, Appl
52	69	80.2	14	2	US-08-709-924-3	Sequence 3, Appli
53	69	80.2	14	2	US-08-709-925-3	Sequence 3, Appli
54	69	80.2	14	4	US-08-709-948-3	Sequence 3, Appli
55	69	80.2	114	4	US-08-918-288-71	Sequence 71, Appl
56	69	80.2	114	4	US-09-282-357-71	Sequence 71, Appl
57	69	80.2	234	4	US-08-918-288-9	Sequence 9, Appli
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59	67	77.9	13	2	US-08-709-924-6	Sequence 6, Appli
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61	67	77.9	13	4	US-08-709-948-6	Sequence 6, Appli
62	67	77.9	14	2	US-08-709-924-18	Sequence 18, Appl
63	67	77.9	14	2	US-08-709-924-26	Sequence 26, Appl
64	67	77.9	14	2	US-08-709-925-18	Sequence 18, Appl
65	67	77.9	14	2	US-08-709-925-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-08-918-388-70
; Sequence 70, Application US/08918288
; Patent No. 6238890
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,288
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/282,357
; FILING DATE:
; APPLICATION NUMBER: 08/853,524

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; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 08/199,382
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20050.25
; TELEPHONE: 202-887-1500
; TELEFAX: 202-887-0763
; TELEX:
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-918-288-70

Query Match 100.0%; Score 86; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLOGVLPALPQVVC 17
Db 41 MTRVLOGVLPALPQVVC 57

RESULT 2
US-09-282-357-70
; Sequence 70, Application US/09282357
; Patent No. 6242580
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/282,357
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/918,288
; FILING DATE: 25 AUG-1997
; APPLICATION NUMBER: 08/853,524
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 08/199,382
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20050.25
; TELEPHONE: 202-887-1500
; TELEFAX: 202-887-0763
; TELEX:
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-282-357-70

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Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLOGVLPALPQVVC 17
Db 41 MTRVLOGVLPALPQVVC 57

RESULT 3
US-08-425-673-7
; Sequence 7, Application US/08425673
; Patent No. 5508261
; GENERAL INFORMATION:
; APPLICANT: Moyle, William R.
; APPLICANT: Campbell, Robert K.
; TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
; TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
; TITLE OF INVENTION: Methods For Preparing and Using Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: P.O. Box 1267
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08551
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,673
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/717,151
; FILING DATE: 18-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Muccino, Richard R.
; REGISTRATION NUMBER: 32,538
; REFERENCE/DOCKET NUMBER: UMD 1.0-004
; TELEPHONE: (609) 466-3407
; TELEFAX: (609) 466-2760
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-425-673-7

Query Match 100.0%; Score 86; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLOGVLPALPQVVC 17
Db 41 MTRVLOGVLPALPQVVC 57

RESULT 4
US-08-425-673-8
; Sequence 8, Application US/08425673
; Patent No. 5508261
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; GENERAL INFORMATION:
; APPLICANT: Moyle, William R.
; TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
; TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
; TITLE OF INVENTION: Methods For Preparing and Using Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: P.O. Box 1267
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08551
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,673
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/717,151
; FILING DATE: 18-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Muccino, Richard R.
; REGISTRATION NUMBER: 32,538
; REFERENCE/DOCKET NUMBER: UMD 1.0-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 466-3407
; TELEFAX: (609) 466-2760
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-425-673-8

Query Match 100.0%; Score 86; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 41 MTRVLQGVLPALPQVVC 57

RESULT 5
US-08-425-673-9
; Sequence 9, Application US/08425673
; Patent No. 5508261
; GENERAL INFORMATION:
; APPLICANT: Moyle, William R.
; APPLICANT: Campbell, Robert K.
; TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
; TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
; TITLE OF INVENTION: Methods For Preparing and Using Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: P.O. Box 1267
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08551
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,673
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/717,151
; FILING DATE: 18-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Muccino, Richard R.
; REGISTRATION NUMBER: 32,538
; REFERENCE/DOCKET NUMBER: UMD 1.0-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 466-3407
; TELEFAX: (609) 466-2760
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-425-673-9

Query Match 100.0%; Score 86; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 6.5e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 41 MTRVLQGVLPALPQVVC 57

RESULT 6
US-08-918-288-69
; Sequence 69, Application US/08918288
; Patent No. 6238890
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,288
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/282,357
; FILING DATE:
; APPLICATION NUMBER: 08/853,524
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 08/199,382
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20050.25
; TELECOMMUNICATION INFORMATION:
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TELEPHONE: 202-887-1500
 TELEFAX: 202-887-0763
 TELEX:
 INFORMATION FOR SEQ ID NO: 69:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 114 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-918-288-69

Query Match 100.0%; Score 86; DB 4; Length 114;
 Best Local Similarity 100.0%; Pred. No. 6.5e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
 Db 41 MTRVLQGVLPALPQVVC 57

RESULT 7

US-09-282-357-69
 Sequence 69, Application US/09282357
 Patent No. 6242580
 GENERAL INFORMATION:
 APPLICANT: BOIME, Irving
 APPLICANT: MOYLE, William R.
 TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
 TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
 NUMBER OF SEQUENCES: 83
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FOERSTER
 STREET: 2000 Pennsylvania Avenue, NW, suite 5500
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20006-1888

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/282.357
 FILING DATE:

CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/918,288
 FILING DATE: 25 AUG-1997
 APPLICATION NUMBER: 08/853,524
 FILING DATE: 09-MAY-1997
 APPLICATION NUMBER: 08/199,382
 FILING DATE: 18-FEB-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Murashige, Kate H
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 29500-20050.25
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-887-1500
 TELEFAX: 202-887-0763
 TELEX:

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:
 LENGTH: 114 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-282-357-69

Query Match 100.0%; Score 86; DB 4; Length 114;
 Best Local Similarity 100.0%; Pred. No. 6.5e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
 Db 41 MTRVLQGVLPALPQVVC 57

RESULT 8

US-08-425-673-11
 Sequence 11, Application US/08425673
 Patent No. 5508261

GENERAL INFORMATION:
 APPLICANT: Moyle, William R.
 APPLICANT: Campbell, Robert K.
 TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
 TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
 TITLE OF INVENTION: Methods For Preparing and Using Same
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Richard R. Muccino
 STREET: P.O. Box 1267
 CITY: Princeton
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 08551

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/425,673
 FILING DATE:

CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/717,151
 FILING DATE: 18-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Muccino, Richard R.

REGISTRATION NUMBER: 32,538
 REFERENCE/DOCKET NUMBER: UMD 1.0-004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (609) 466-3407
 TELEFAX: (609) 466-2760
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 117 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-425-673-11

Query Match 100.0%; Score 86; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 6.6e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
 Db 41 MTRVLQGVLPALPQVVC 57

RESULT 9

US-08-425-673-12
 Sequence 12, Application US/08425673
 Patent No. 5508261

GENERAL INFORMATION:

APPLICANT: Moyle, William R.
 APPLICANT: Campbell, Robert K.
 TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
 TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
 TITLE OF INVENTION: Methods For Preparing and Using Same
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:


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Query Match      100.0%; Score 86; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
   |||||
Db 41 MTRVLQGVLPALPQVVC 57

RESULT 12
US-08-425-673-10
; Sequence 10, Application US/08425673
; Patent No. 5508261
; GENERAL INFORMATION:
; APPLICANT: Moyle, William R.
; TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
; TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
; TITLE OF INVENTION: Methods For Preparing and Using Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: P.O. Box 1267
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08551
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,673
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/717,151
; FILING DATE: 18-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Muccino, Richard R.
; REGISTRATION NUMBER: 32,538
; REFERENCE/DOCKET NUMBER: UMD 1.0-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 466-3407
; TELEFAX: (609) 466-2760
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-425-673-10

Query Match      100.0%; Score 86; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
   |||||
Db 41 MTRVLQGVLPALPQVVC 57

RESULT 13
US-08-298-189B-1
; Sequence 1, Application US/08298189B
; Patent No. 5674727
; GENERAL INFORMATION:
; APPLICANT: Dr. Laurence A. Cole and Dr. Andrew Kardana
; TITLE OF INVENTION: No. 5674727el Methods for Detecting Reproductive
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; TITLE OF INVENTION: Cancers or Tumors and Assay Products
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Laurence A. Cole, c/o Dept. of Obstetrics and
; STREET: 333 Cedar Street
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06510
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Microsoft Word 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/298,189B
; FILING DATE: 08/31/94
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brian D. Voyce
; REGISTRATION NUMBER: 28,917
; REFERENCE/DOCKET NUMBER: DS11
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-638-3939 or 803-272-1471
; TELEFAX: 919-638-3939 or 803-272-1471
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. 5674727 applicable
; TOPOLOGY: Unknown
; MOLECULE TYPE: subunit of hormone, specifically the
; MOLECULE TYPE: beta subunit of hCG
; ORIGINAL SOURCE: human urine
; FEATURE:
; NAME/KEY: beta subunit of hCG that is nicked by GBNE
; LOCATION: hCG
; IDENTIFICATION METHOD: N-terminal sequence analysis
; PUBLICATION INFORMATION:
; AUTHORS: Keutmann et alia
; TITLE: "A Receptor-binding Region in Human
; JOURNAL: Proc Nat'l Acad Sci USA
; VOLUME: 84
; ISSUE: No. 5674727 applicable
; PAGES: 2038-2042
; DATE: 1987
; US-08-298-189B-1

Query Match      100.0%; Score 86; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
   |||||
Db 41 MTRVLQGVLPALPQVVC 57

RESULT 14
US-08-475-213-10
; Sequence 10, Application US/08475213
; Patent No. 5783674
; GENERAL INFORMATION:
; APPLICANT: Geysen, Hendrik M.
; TITLE OF INVENTION: Method for the use and Synthesis of
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
```


ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,213
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/752,437
FILING DATE: 06-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO pct/au90/00062
FILING DATE: 16-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ2788/89
FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31259
REFERENCE/DOCKET NUMBER: 0240.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-475-213-10

Query Match 100.0%; Score 86; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 41 MTRVLQGVLPALPQVVC 57

RESULT 15
US-08-395-238-2
Sequence 2, Application US/08395238
Patent No. 586488
GENERAL INFORMATION:
APPLICANT: ISSACS, Neil William
APPLICANT: LAPHORN, Adrian Jonathan
APPLICANT: HARRIS, Deborah Claire
TITLE OF INVENTION: THREE DIMENSIONAL HORMONE STRUCTURE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: AKZO NOBEL PATENT DEPARTMENT
STREET: 1300 PICCARD DRIVE, SUITE 206
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: UNITED STATES
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/395,238
FILING DATE: 24-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9403600.1
FILING DATE: 24-FEB-1994
ATTORNEY/AGENT INFORMATION:

NAME: WILLIAM M. BLACKSTONE
REGISTRATION NUMBER: 29,722
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BETA-SUBUNIT HUMAN CHORIONIC GONADOTROPIN
US-08-395-238-2

Query Match 100.0%; Score 86; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 41 MTRVLQGVLPALPQVVC 57

RESULT 16
US-09-142-320-4
Sequence 4, Application US/09142320
Patent No. 6194154
GENERAL INFORMATION:
APPLICANT: Bellet, Dominique
APPLICANT: Bidart, Jean-Michel
APPLICANT: Vidaud, Michel
APPLICANT: Lazar, Vladimir
TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION DETECTION METHOD
FILE REFERENCE: 065691/0140
CURRENT APPLICATION NUMBER: US/09/142,320
CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/FR97/00361
EARLIER FILING DATE: 1997-02-28
EARLIER APPLICATION NUMBER: FR 96 02683
EARLIER FILING DATE: 1996-03-04
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 145
TYPE: PRT
ORGANISM: human
FEATURE:
OTHER INFORMATION: consensus sequence
FEATURE:
OTHER INFORMATION: Xaa at position 2 is a Lys or Arg
FEATURE:
OTHER INFORMATION: Xaa at position 4 is a Pro or Met
FEATURE:
OTHER INFORMATION: Xaa at position 117 is an Ala or Asp
US-09-142-320-4

Query Match 100.0%; Score 86; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 41 MTRVLQGVLPALPQVVC 57

RESULT 17
US-09-142-320-11
Sequence 11, Application US/09142320
Patent No. 6194154
GENERAL INFORMATION:
APPLICANT: Bellet, Dominique

```
; APPLICANT: Bidart, Jean-Michel
; APPLICANT: Vidaud, Vladimir
; APPLICANT: Lazar, Vladimir
; TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION DETECTION METHOD
; FILE REFERENCE: 065691/0140
; CURRENT APPLICATION NUMBER: US/09/142,320
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/FR97/00361
; EARLIER FILING DATE: 1997-02-28
; EARLIER APPLICATION NUMBER: FR 96 02683
; EARLIER FILING DATE: 1996-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 145
; TYPE: PRT
; ORGANISM: human
US-09-142-320-11

Query Match          100.0%; Score 86; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLOGVLPALPQVVC 17
Db 41 MTRVLOGVLPALPQVVC 57

RESULT 18
US-09-142-320-12
; Sequence 12, Application US/09142320
; Patent No. 6194154
; GENERAL INFORMATION:
; APPLICANT: Bellet, Dominique
; APPLICANT: Bidart, Jean-Michel
; APPLICANT: Vidaud, Michel
; APPLICANT: Lazar, Vladimir
; TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION DETECTION METHOD
; FILE REFERENCE: 065691/0140
; CURRENT APPLICATION NUMBER: US/09/142,320
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/FR97/00361
; EARLIER FILING DATE: 1997-02-28
; EARLIER APPLICATION NUMBER: FR 96 02683
; EARLIER FILING DATE: 1996-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 145
; TYPE: PRT
; ORGANISM: human
US-09-142-320-12

Query Match          100.0%; Score 86; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLOGVLPALPQVVC 17
Db 41 MTRVLOGVLPALPQVVC 57

RESULT 19
US-09-142-320-13
; Sequence 13, Application US/09142320
; Patent No. 6194154
; GENERAL INFORMATION:
; APPLICANT: Bellet, Dominique
; APPLICANT: Bidart, Jean-Michel
; APPLICANT: Vidaud, Michel
; APPLICANT: Lazar, Vladimir
; TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION DETECTION METHOD
; FILE REFERENCE: 065691/0140
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; CURRENT APPLICATION NUMBER: US/09/142,320
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/FR97/00361
; EARLIER FILING DATE: 1997-02-28
; EARLIER APPLICATION NUMBER: FR 96 02683
; EARLIER FILING DATE: 1996-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 145
; TYPE: PRT
; ORGANISM: human
US-09-142-320-13

Query Match          100.0%; Score 86; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLOGVLPALPQVVC 17
Db 41 MTRVLOGVLPALPQVVC 57

RESULT 20
US-09-142-320-14
; Sequence 14, Application US/09142320
; Patent No. 6194154
; GENERAL INFORMATION:
; APPLICANT: Bellet, Dominique
; APPLICANT: Bidart, Jean-Michel
; APPLICANT: Vidaud, Michel
; APPLICANT: Lazar, Vladimir
; TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION DETECTION METHOD
; FILE REFERENCE: 065691/0140
; CURRENT APPLICATION NUMBER: US/09/142,320
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/FR97/00361
; EARLIER FILING DATE: 1997-02-28
; EARLIER APPLICATION NUMBER: FR 96 02683
; EARLIER FILING DATE: 1996-03-04
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 145
; TYPE: PRT
; ORGANISM: human
US-09-142-320-14

Query Match          100.0%; Score 86; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLOGVLPALPQVVC 17
Db 41 MTRVLOGVLPALPQVVC 57

RESULT 21
US-09-142-320-15
; Sequence 15, Application US/09142320
; Patent No. 6194154
; GENERAL INFORMATION:
; APPLICANT: Bellet, Dominique
; APPLICANT: Bidart, Jean-Michel
; APPLICANT: Vidaud, Michel
; APPLICANT: Lazar, Vladimir
; TITLE OF INVENTION: MALIGNANT HUMAN CELL TRANSFORMATION DETECTION METHOD
; FILE REFERENCE: 065691/0140
; CURRENT APPLICATION NUMBER: US/09/142,320
; CURRENT FILING DATE: 1998-09-04
; EARLIER APPLICATION NUMBER: PCT/FR97/00361
; EARLIER FILING DATE: 1997-02-28
; EARLIER APPLICATION NUMBER: FR 96 02683
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REFERENCE/DOCKET NUMBER: 29500-20050.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-887-0763
TELEX:
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-282-357-68

Query Match 100.0%; Score 86; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLOGVLPALPQVVC 17
|||||

Db 41 MTRVLOGVLPALPQVVC 57

RESULT 25

US-08-908-371B-1
Sequence 1, Application US/08908371B
Patent No. 6331610

GENERAL INFORMATION:

APPLICANT: Bourinbalar, Aldar S.
TITLE OF INVENTION: A Method for Preventing and Treating
TITLE OF INVENTION: AIDS and HIV Infection Using Select Peptides From the
TITLE OF INVENTION: Beta Subunit of Human Chorionic Gonadotropin
NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Metatron, Inc.
STREET: 367 Bay Shore Road
CITY: Deer Park
STATE: New York
COUNTRY: United States of America
ZIP: 11729

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 in. diskette (1.44megabytes)
COMPUTER: IBM Compatible PC
OPERATING SYSTEM: Windows 95
SOFTWARE: WORD 6.0 ASCII TEXT CONVERSION ONLY

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/908,371B
FILING DATE: 07-AUG-1997
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/044,937
FILING DATE: 25-APR-1997

ATTORNEY/AGENT INFORMATION:

NAME: COLEMAN, HENRY D.
REGISTRATION NUMBER: 32,559
REFERENCE/DOCKET NUMBER: M31-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 679-0090
TELEFAX: (212) 679-9121

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 145 Amino Acid Units
TYPE: Amino Acid
STRANDEDNESS: Single Stranded
TOPOLOGY: Linear
MOLECULE TYPE: Protein Subunit
DESCRIPTION: Amino Acid Corresponding to Beta Subunit
DESCRIPTION: of Human Chorionic Gonadotropin
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE: Sequence
IMMEDIATE SOURCE: N/A
POSITION IN GENOME: N/A
FEATURE:

NAME/KEY: 145 Units of Beta Subunit of Human Chorionic
NAME/KEY: Gonadotropin
LOCATION: N/A
IDENTIFICATION METHOD: Sequencing
PUBLICATION INFORMATION:
AUTHORS: CARLSEN, Robert B.,
AUTHORS: BAHL, Ohm P.,
AUTHORS: SWAMINATHAN, N.
TITLE: HUMAN CHORIONIC GONADOTROPIN
JOURNAL: THE JOURNAL OF BIOLOGICAL CHEMISTRY
VOLUME: 248
PAGES: 6810-6825
DATE: 1973

US-08-908-371B-1

Query Match 100.0%; Score 86; DB 4; Length 145;
Best Local Similarity 100.0%; Pred. No. 8.4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLOGVLPALPQVVC 17
|||||

Db 41 MTRVLOGVLPALPQVVC 57

Search completed: December 4, 2002, 11:29:14
Job time: 15.45 secs

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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:27:25 ; Search time 8.5 Seconds
(without alignments)

32.485 Million cell updates/sec

Title: US-09-821-380-1

Perfect score: 86

Sequence: 1 MTRVLQGLPALPQWC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database :

Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	86	100.0	17	10	US-09-821-380-1
2	86	100.0	20	9	US-09-915-676-9
3	86	100.0	20	10	US-09-466-320-6
4	86	100.0	141	9	US-09-813-398-3
5	86	100.0	165	9	US-09-915-676-1
6	86	100.0	165	10	US-09-466-320-14
7	86	100.0	195	10	US-09-780-933-30
8	86	100.0	196	10	US-09-780-933-29
9	86	100.0	307	10	US-09-756-186-4
10	86	100.0	336	10	US-09-756-186-8
11	69	80.2	122	9	US-09-813-398-4
12	67	77.9	13	10	US-09-821-380-2
13	55	64.0	113	10	US-09-730-617-44
14	52	60.5	10	10	US-09-821-380-3
15	50	58.1	10	10	US-09-821-380-4
16	50	58.1	99	10	US-09-730-617-41
17	50	58.1	141	10	US-09-730-617-47
18	50	58.1	141	10	US-09-730-617-48
19	43	50.0	65	10	US-09-764-860-467

20	41	47.7	8	10	US-09-821-380-10	Sequence 10, Appl
21	41	47.7	260	10	US-09-731-231A-5	Sequence 5, Appl
22	40	46.5	74	10	US-09-864-761-33496	Sequence 33496, A
23	40	46.5	416	10	US-09-731-231A-6	Sequence 6, Appl
24	40	46.5	622	9	US-09-981-353-129	Sequence 129, App
25	40	46.5	3594	10	US-09-911-842-4	Sequence 4, Appl
26	39	45.3	214	10	US-09-995-515-5	Sequence 5, Appl
27	39	45.3	364	9	US-10-066-500-65	Sequence 65, Appl
28	39	45.3	364	12	US-10-117-178-2	Sequence 2, Appl
29	38	44.2	55	10	US-09-864-761-41625	Sequence 41625, A
30	38	44.2	236	10	US-09-925-300-1410	Sequence 1410, Ap
31	38	44.2	333	10	US-09-769-159-2	Sequence 2, Appl
32	38	44.2	333	10	US-09-848-889-1	Sequence 1, Appl
33	38	44.2	623	9	US-09-792-630-5	Sequence 5, Appl
34	38	44.2	623	9	US-09-792-630-7	Sequence 7, Appl
35	38	44.2	623	9	US-10-080-376-5	Sequence 5, Appl
36	38	44.2	623	9	US-10-080-376-7	Sequence 7, Appl
37	38	44.2	624	9	US-09-792-630-9	Sequence 9, Appl
38	38	44.2	624	9	US-10-080-376-9	Sequence 9, Appl
39	38	44.2	685	10	US-09-771-161A-249	Sequence 249, App
40	38	44.2	685	10	US-09-771-161A-250	Sequence 250, App
41	38	44.2	685	10	US-09-771-161A-251	Sequence 251, App
42	38	44.2	1288	9	US-09-736-968A-13	Sequence 13, Appl
43	38	44.2	1288	10	US-09-736-969A-13	Sequence 13, Appl
44	38	44.2	1288	10	US-09-736-969A-13	Sequence 13, Appl
45	38	44.2	2180	9	US-09-736-968A-110	Sequence 110, App
46	38	44.2	2180	10	US-09-736-969A-96	Sequence 96, Appl
47	38	44.2	2180	10	US-09-736-960-93	Sequence 93, Appl
48	37	43.0	125	10	US-09-867-550-658	Sequence 658, App
49	37	43.0	318	10	US-09-925-302-564	Sequence 564, App
50	37	43.0	470	9	US-10-006-950-2	Sequence 2, Appl
51	37	43.0	470	10	US-09-805-467A-2	Sequence 2, Appl
52	37	43.0	654	10	US-09-969-528-10	Sequence 10, Appl
53	37	43.0	928	10	US-09-801-574-44	Sequence 44, Appl
54	36	41.9	7	10	US-09-821-380-11	Sequence 11, Appl
55	36	41.9	114	10	US-09-925-300-1551	Sequence 1551, Ap
56	36	41.9	129	10	US-09-791-171-149	Sequence 149, App
57	36	41.9	254	9	US-10-104-019-19	Sequence 19, Appl
58	36	41.9	279	10	US-09-775-879-23	Sequence 23, Appl
59	36	41.9	301	9	US-09-758-017A-2	Sequence 2, Appl
60	36	41.9	329	10	US-09-725-285-9	Sequence 9, Appl
61	36	41.9	329	10	US-09-195-662A-9	Sequence 9, Appl
62	36	41.9	329	10	US-09-339-912A-9	Sequence 9, Appl
63	36	41.9	329	10	US-09-502-783A-9	Sequence 9, Appl
64	36	41.9	334	10	US-09-747-835A-32	Sequence 32, Appl
65	36	41.9	344	10	US-09-779-879A-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-09-821-380-1
; Sequence 1, Application US/09821380
; Patent No. US20020064501A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Ahmed
; APPLICANT: Benner, Robert
; APPLICANT: Savelkoul, Josef
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-47990S
; CURRENT APPLICATION NUMBER: US/09/821,380
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/NL99/00313
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/777,777
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: EP 98201695.8
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Peptide immunoregulator
US-09-821-380-1

Query Match 100.0%; Score 86; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.2e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
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Db 1 MTRVLQGVLPALPQVVC 17

RESULT 2

US-09-915-676-9
; Sequence 9, Application US/09915676
; Patent No. US20020164338A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Combined Approach to Treatment of Cancer
; FILE REFERENCE: 50450-8027.US01
; CURRENT APPLICATION NUMBER: US/09/915,676
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 09/571,497
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/134,419
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/134,432
; PRIOR FILING DATE: 1998-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-676-9

Query Match 100.0%; Score 86; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
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Db 4 MTRVLQGVLPALPQVVC 20

RESULT 3

US-09-466-320-6
; Sequence 6, Application US/09466320
; Patent No. US20020025939A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick
; TITLE OF INVENTION: Chorionic Gonadotropin DNA Vaccines and
; FILE REFERENCE: 0450-0026.30
; CURRENT APPLICATION NUMBER: US/09/466,320
; CURRENT FILING DATE: 1999-12-17
; EARLIER APPLICATION NUMBER: US 60/112,910
; EARLIER FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-466-320-6

Query Match 100.0%; Score 86; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.1e-08;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
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Db 4 MTRVLQGVLPALPQVVC 20

RESULT 4

US-09-813-398-3
; Sequence 3, Application US/09813398
; Patent No. US20020169292A1
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
; APPLICANT: Mariusz W. Szkudlinski
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
; FILE REFERENCE: UOFMD.003C1
; CURRENT APPLICATION NUMBER: US/09/813,398
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/05908
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/19772
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 141
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-09-813-398-3

Query Match 100.0%; Score 86; DB 9; Length 141;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
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Db 42 MTRVLQGVLPALPQVVC 58

RESULT 5

US-09-915-676-1
; Sequence 1, Application US/09915676
; Patent No. US20020164338A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Combined Approach to Treatment of Cancer
; FILE REFERENCE: 50450-8027.US01
; CURRENT APPLICATION NUMBER: US/09/915,676
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 09/571,497
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/134,419
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/134,432
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-676-1

Query Match 100.0%; Score 86; DB 9; Length 165;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17

Db 61 MTRVLQGVLPALPQVVC 77
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RESULT 6
US-09-466-320-14
; Sequence 14, Application US/09466320
; Patent No. US2002002593A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick
; TITLE OF INVENTION: Chorionic Gonadotropin DNA Vaccines and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 0450-0026.30
; CURRENT APPLICATION NUMBER: US/09/466,320
; CURRENT FILING DATE: 1999-12-17
; EARLIER APPLICATION NUMBER: US 60/112,910
; EARLIER FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hcg beta sub unit
US-09-466-320-14

Query Match 100.0%; Score 86; DB 10; Length 165;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
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Db 61 MTRVLQGVLPALPQVVC 77

RESULT 7
US-09-780-933-30
; Sequence 30, Application US/09780933
; Patent No. US20020127652A1
; GENERAL INFORMATION:
; APPLICANT: SCHAMBE, HANS T.
; APPLICANT: ANDERSEN, KIM V.
; APPLICANT: VAN DEN HAZEL, BART
; APPLICANT: CHRISTIANSEN, JESPER
; APPLICANT: JEPPESEN, CLAUS B.
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
; FILE REFERENCE: 31-001000US
; CURRENT APPLICATION NUMBER: US/09/780,933
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PA 2000 00220
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,035
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PA 2000 01092
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,558
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-933-30

Query Match 100.0%; Score 86; DB 10; Length 195;
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
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Db 125 MTRVLQGVLPALPQVVC 141

RESULT 8
US-09-780-933-29
; Sequence 29, Application US/09780933
; Patent No. US20020127652A1
; GENERAL INFORMATION:
; APPLICANT: SCHAMBE, HANS T.
; APPLICANT: ANDERSEN, KIM V.
; APPLICANT: VAN DEN HAZEL, BART
; APPLICANT: CHRISTIANSEN, JESPER
; APPLICANT: JEPPESEN, CLAUS B.
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
; FILE REFERENCE: 31-001000US
; CURRENT APPLICATION NUMBER: US/09/780,933
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PA 2000 00220
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,035
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PA 2000 01092
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,558
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-933-29

Query Match 100.0%; Score 86; DB 10; Length 196;
Best Local Similarity 100.0%; Pred. No. 6.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
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Db 126 MTRVLQGVLPALPQVVC 142

RESULT 9
US-09-756-186-4
; Sequence 4, Application US/09756186
; Patent No. US20010014333A1
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/804,166
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.

; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-730-617-41

Query Match 58.1%; Score 50; DB 10; Length 99;
Best Local Similarity 58.8%; Pred. No. 0.18;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
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DB 41 MKRVLVLPVLPMPQVVC 57

RESULT 17

US-09-730-617-47
; Sequence 47, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:

; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shinkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: NO. US20020068279A1el Proteins and Nucleic Acids Encoding the Sam
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730,617
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-730-617-47

Query Match 58.1%; Score 50; DB 10; Length 141;
Best Local Similarity 58.8%; Pred. No. 0.27;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
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DB 61 MKRVLVLPVLPMPQVVC 77

RESULT 18

US-09-730-617-48
; Sequence 48, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:

; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shinkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: NO. US20020068279A1el Proteins and Nucleic Acids Encoding the Sam
; FILE REFERENCE: 15966-609

; CURRENT APPLICATION NUMBER: US/09/730,617

; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Ovis aries
US-09-730-617-48

Query Match 58.1%; Score 50; DB 10; Length 141;
Best Local Similarity 58.8%; Pred. No. 0.27;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
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DB 61 MKRVLVLPVLPMPQVVC 77

RESULT 19

US-09-764-860-467
; Sequence 467, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-860-467

Query Match 50.0%; Score 43; DB 10; Length 65;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VLQGVLPALP 13
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DB 26 VLSGILPALP 35

RESULT 20

US-09-821-380-10
; Sequence 10, Application US/09821380
; Patent No. US20020064501A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Ahmed
; APPLICANT: Benner, Robbert
; APPLICANT: Savelkoul, Josef
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-4799US
; CURRENT APPLICATION NUMBER: US/09/821,380
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/NL99/00313
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/???,???
; PRIOR FILING DATE: 2000-11-20

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; PRIOR APPLICATION NUMBER: EP 98201695.8
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fragment of peptide immunoregulator
US-09-821-380-10

Query Match 47.7%; Score 41; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.6e+04; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

QY 7 GVLPALPQ 14
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Db 1 GVLPALPQ 8

RESULT 21
US-09-731-231A-5
; Sequence 5, Application US/09731231A
; Patent No. US20020082189A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; FILE REFERENCE: CL001007
; CURRENT APPLICATION NUMBER: US/09/731,231A
; CURRENT FILING DATE: 2000-12-07
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 5
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Human
US-09-731-231A-5

Query Match 47.7%; Score 41; DB 10; Length 260;
Best Local Similarity 50.0%; Pred. No. 15;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 RVLGVLPALPQ 14
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Db 212 RIIEGKLPMR 223

RESULT 22
US-09-864-761-33496
; Sequence 33496, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
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; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33496
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL035541.12
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.84
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 20
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 19
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
; OTHER INFORMATION: EST_HUMAN HIT: R86197.1, EVALUE 4.00e-37
; OTHER INFORMATION: SWISSPROT HIT: P35558, EVALUE 1.00e-38
US-09-864-761-33496

Query Match 46.5%; Score 40; DB 10; Length 74;
Best Local Similarity 57.1%; Pred. No. 5.2;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RVLGVLPALPQV 16
|:|:| |
Db 14 KVVQGLSLPQAV 27

RESULT 23
US-09-731-231A-6
; Sequence 6, Application US/09731231A
; Patent No. US20020082189A1
; GENERAL INFORMATION:
; APPLICANT: GUEGLER, Karl et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001007
; CURRENT APPLICATION NUMBER: US/09/731,231A
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Mus musculus
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US-09-731-231A-6

Query Match 46.5%; Score 40; DB 10; Length 416;
Best Local Similarity 46.2%; Pred. No. 37;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 RVLQGVLPALPQV 15
|:::| |::|
Db 212 RIIEGKLPPMPKV 224

RESULT 24

US-09-981-353-129
; Sequence 129, Application US/09981353
; Patent No. US20020160382A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
; FILE REFERENCE: PA-0038 US
; CURRENT APPLICATION NUMBER: US/09/981,353
; CURRENT FILING DATE: 2001-10-11
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 129
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 1843408CD1
US-09-981-353-129

Query Match 46.5%; Score 40; DB 9; Length 622;
Best Local Similarity 57.1%; Pred. No. 58;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 RVLQGVLPALPQV 16
:|::| |::|
Db 14 KVVQGSLSLPQAV 27

RESULT 25

US-09-911-842-4
; Sequence 4, Application US/09911842
; Patent No. US20020151483A1
; GENERAL INFORMATION:
; APPLICANT: Welch, Andrew A.
; APPLICANT: Elliott, Gary S.
; TITLE OF INVENTION: C3H/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37592
; CURRENT APPLICATION NUMBER: US/09/911,842
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: US 60/222,438
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 3594
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1757)..()
; OTHER INFORMATION: Xaa = any or unknown amino acid
US-09-911-842-4

Query Match 46.5%; Score 40; DB 10; Length 3594;
Best Local Similarity 57.1%; Pred. No. 4.2e+02;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 VLOGVLPALPQVVC 17
:| | | | | | | |

Db 1466 LLDGVLP TLHATC 1479

Search completed: December 4, 2002, 11:37:18
Job time : 9.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:26:10 ; Search time 176.375 Seconds
(without alignments)
62.143 Million cell updates/sec

Title: US-09-821-380-1

Perfect score: 86

Sequence: 1 MTRVLQGVLPALPQVVC 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database :

Pending_Patents_AA_Main:*

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- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US08_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
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- 23: /cgn2_6/ptodata/1/paa/US099_COMB.pep.*
- 24: /cgn2_6/ptodata/1/paa/US100_COMB.pep.*
- 25: /cgn2_6/ptodata/1/paa/US101_COMB.pep.*
- 26: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
- 27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	17	22	US-09-821-380-1
2	86	100.0	20	1	PCT-US00-27741-3
3	86	100.0	20	1	PCT-US00-27741-5
4	86	100.0	20	1	PCT-US00-27741-23
5	86	100.0	20	8	US-08-406-916B-25
6	86	100.0	20	18	US-09-413-564-3

7	86	100.0	20	18	US-09-413-564-5	Sequence 5, Appli
8	86	100.0	20	18	US-09-413-564-23	Sequence 23, Appl
9	86	100.0	20	18	US-09-413-564A-18	Sequence 38, Appl
10	86	100.0	20	18	US-09-413-564A-38	Sequence 18, Appl
11	86	100.0	20	18	US-09-413-564A-40	Sequence 40, Appl
12	86	100.0	20	18	US-09-413-564C-18	Sequence 18, Appl
13	86	100.0	20	18	US-09-413-564C-38	Sequence 38, Appl
14	86	100.0	20	18	US-09-413-564C-40	Sequence 40, Appl
15	86	100.0	20	18	US-09-466-320-6	Sequence 6, Appli
16	86	100.0	20	19	US-09-571-497-9	Sequence 9, Appli
17	86	100.0	20	21	US-09-766-397B-6	Sequence 6, Appli
18	86	100.0	20	23	US-09-915-676-9	Sequence 9, Appli
19	86	100.0	24	19	US-09-587-223A-37	Sequence 37, Appl
20	86	100.0	24	19	US-09-587-223A-95	Sequence 59, Appl
21	86	100.0	25	19	US-09-587-223A-59	Sequence 4, Appli
22	86	100.0	27	1	PCT-US00-27741-4	Sequence 6, Appli
23	86	100.0	27	18	US-09-413-564-6	Sequence 4, Appli
24	86	100.0	27	18	US-09-413-564-4	Sequence 6, Appli
25	86	100.0	27	18	US-09-413-564A-33	Sequence 33, Appl
26	86	100.0	27	18	US-09-413-564A-41	Sequence 41, Appl
27	86	100.0	27	18	US-09-413-564C-33	Sequence 33, Appl
28	86	100.0	27	18	US-09-413-564C-41	Sequence 41, Appl
29	86	100.0	27	18	US-09-413-564C-41	Sequence 41, Appl
30	86	100.0	58	27	US-60-177-571-4490	Sequence 4490, Ap
31	86	100.0	62	27	US-60-182-467-1728	Sequence 1728, Ap
32	86	100.0	75	27	US-60-182-467-1727	Sequence 1727, Ap
33	86	100.0	79	27	US-60-182-467-1729	Sequence 1729, Ap
34	86	100.0	82	20	US-09-654-923-13	Sequence 13, Appl
35	86	100.0	93	12	US-08-853-524-70	Sequence 70, Appl
36	86	100.0	93	12	US-08-853-524-27	Sequence 27, Appl
37	86	100.0	107	23	US-09-927-876-33	Sequence 33, Appl
38	86	100.0	109	23	US-09-927-876-38	Sequence 38, Appl
39	86	100.0	114	5	US-08-108-845-7	Sequence 7, Appli
40	86	100.0	114	5	US-08-108-845-8	Sequence 8, Appli
41	86	100.0	114	5	US-08-108-845-9	Sequence 9, Appli
42	86	100.0	114	12	US-08-853-524-69	Sequence 69, Appl
43	86	100.0	114	12	US-08-867-587-26	Sequence 26, Appl
44	86	100.0	114	27	US-60-196-718-5933	Sequence 5933, Ap
45	86	100.0	117	5	US-08-108-845-11	Sequence 11, Appl
46	86	100.0	117	5	US-08-108-845-12	Sequence 12, Appl
47	86	100.0	134	27	US-60-196-718-5932	Sequence 5932, Ap
48	86	100.0	141	22	US-09-813-398-3	Sequence 3, Appli
49	86	100.0	142	15	US-09-104-400-136	Sequence 136, App
50	86	100.0	144	3	US-07-971-842-61	Sequence 61, Appl
51	86	100.0	145	1	PCT-US00-27741-1	Sequence 1, Appli
52	86	100.0	145	5	US-08-108-845-1	Sequence 1, Appli
53	86	100.0	145	5	US-08-108-845-2	Sequence 2, Appli
54	86	100.0	145	5	US-08-108-845-10	Sequence 10, Appl
55	86	100.0	145	8	US-08-406-916B-8	Sequence 8, Appli
56	86	100.0	145	12	US-08-853-524-68	Sequence 68, Appl
57	86	100.0	145	12	US-08-867-587-25	Sequence 25, Appl
58	86	100.0	145	15	US-09-104-400-2	Sequence 2, Appli
59	86	100.0	145	16	US-09-206-137-53	Sequence 53, Appl
60	86	100.0	145	18	US-09-413-564-1	Sequence 1, Appli
61	86	100.0	145	18	US-09-413-564A-1	Sequence 1, Appli
62	86	100.0	145	18	US-09-413-564C-1	Sequence 1, Appli
63	86	100.0	145	21	US-09-760-294-4	Sequence 4, Appli
64	86	100.0	145	21	US-09-760-294-11	Sequence 11, Appl
65	86	100.0	145	21	US-09-760-294-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1

US-09-821-380-1
; Sequence 1, Application US/09821380
; GENERAL INFORMATION:
; APPLICANT: Khan, Ahmed
; APPLICANT: Benner, Robbert
; APPLICANT: Saveikoul, Josef
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-4799US

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; CURRENT APPLICATION NUMBER: US/09/821.380
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/NL99/00313
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/???
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: EP 98201695.8
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Peptide immunoregulator
US-09-821-380-1

Query Match          100.0%; Score 86; DB 22; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLOGVLPALPQVVC 17
Db 1 MTRVLOGVLPALPQVVC 17

RESULT 2
PCT-US00-27741-3
; Sequence 3, Application PC/TUS0027741
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; TITLE OF INVENTION: Antigenic Modification of Polypeptides
; FILE REFERENCE: URF 2-056 AVPCT
; CURRENT APPLICATION NUMBER: PCT/US00/27741
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
PCT-US00-27741-3

Query Match          100.0%; Score 86; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLOGVLPALPQVVC 17
Db 4 MTRVLOGVLPALPQVVC 20

RESULT 3
PCT-US00-27741-5
; Sequence 5, Application PC/TUS0027741
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; TITLE OF INVENTION: Antigenic Modification of Polypeptides
; FILE REFERENCE: URF 2-056 AVPCT
; CURRENT APPLICATION NUMBER: PCT/US00/27741
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
PCT-US00-27741-5

Query Match          100.0%; Score 86; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLOGVLPALPQVVC 17
Db 4 MTRVLOGVLPALPQVVC 20

RESULT 4
PCT-US00-27741-23
; Sequence 23, Application PC/TUS0027741
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; TITLE OF INVENTION: Antigenic Modification of Polypeptides
; FILE REFERENCE: URF 2-056 AVPCT
; CURRENT APPLICATION NUMBER: PCT/US00/27741
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
PCT-US00-27741-23

Query Match          100.0%; Score 86; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLOGVLPALPQVVC 17
Db 4 MTRVLOGVLPALPQVVC 20

RESULT 5
US-08-406-916B-25
; Sequence 25, Application US/08406916B
; GENERAL INFORMATION:
; APPLICANT: STEVENS, VERNON C.
; TITLE OF INVENTION: VACCINES AND ANTIGENIC CONJUGATES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLARD, SIDNEY W.
; STREET: 7632 SLATE RIDGE BOULEVARD
; CITY: REYNOLDSBURG
; STATE: OHIO
; COUNTRY: USA
; ZIP: 43068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
; COMPUTER: IBM PS/2 COMPATIBLE 486 DX 33
; OPERATING SYSTEM: MS DOS 6.2
; SOFTWARE: WORDPERFECT FOR MS DOS 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,916B
; FILING DATE: 27 MAR 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/08370
; FILING DATE: 30 SEP 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KREMBLAS, FRANCIS T., JR.
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
PCT-US00-27741-5

Query Match          100.0%; Score 86; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLOGVLPALPQVVC 17
Db 4 MTRVLOGVLPALPQVVC 20

RESULT 4
PCT-US00-27741-23
; Sequence 23, Application PC/TUS0027741
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; TITLE OF INVENTION: Antigenic Modification of Polypeptides
; FILE REFERENCE: URF 2-056 AVPCT
; CURRENT APPLICATION NUMBER: PCT/US00/27741
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
PCT-US00-27741-23

Query Match          100.0%; Score 86; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLOGVLPALPQVVC 17
Db 4 MTRVLOGVLPALPQVVC 20

RESULT 5
US-08-406-916B-25
; Sequence 25, Application US/08406916B
; GENERAL INFORMATION:
; APPLICANT: STEVENS, VERNON C.
; TITLE OF INVENTION: VACCINES AND ANTIGENIC CONJUGATES
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLARD, SIDNEY W.
; STREET: 7632 SLATE RIDGE BOULEVARD
; CITY: REYNOLDSBURG
; STATE: OHIO
; COUNTRY: USA
; ZIP: 43068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB
; COMPUTER: IBM PS/2 COMPATIBLE 486 DX 33
; OPERATING SYSTEM: MS DOS 6.2
; SOFTWARE: WORDPERFECT FOR MS DOS 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,916B
; FILING DATE: 27 MAR 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/08370
; FILING DATE: 30 SEP 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KREMBLAS, FRANCIS T., JR.
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;
; REGISTRATION NUMBER: 22,773
; REFERENCE/DOCKET NUMBER: URF 2 056 3 3 3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (614) 575 2100
; TELEFAX: (614) 575 2149
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: 38-57 linear fragment of human HCG
; FEATURE:
; LOCATION: the 38-57 linear fragment can be found in SEQ ID
; LOCATION: NO: 8, HCG
; OTHER INFORMATION: when modified, provides immunogenic activity
US-08-406-916B-25

Query Match 100.0%; Score 86; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRVLOGVLPALPQVVC 17
Db 4 MTRVLOGVLPALPQVVC 20

RESULT 6
US-09-413-564-3
; Sequence 3, Application US/09413564
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; APPLICANT: Stevens, Vernon
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564
; CURRENT FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
US-09-413-564-3

Query Match 100.0%; Score 86; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRVLOGVLPALPQVVC 17
Db 4 MTRVLOGVLPALPQVVC 20

RESULT 7
US-09-413-564-5
; Sequence 5, Application US/09413564
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; APPLICANT: Stevens, Vernon
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564
; CURRENT FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
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;
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
US-09-413-564-5

Query Match 100.0%; Score 86; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRVLOGVLPALPQVVC 17
Db 4 MTRVLOGVLPALPQVVC 20

RESULT 8
US-09-413-564-23
; Sequence 23, Application US/09413564
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; APPLICANT: Stevens, Vernon
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564
; CURRENT FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
US-09-413-564-23

Query Match 100.0%; Score 86; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTRVLOGVLPALPQVVC 17
Db 4 MTRVLOGVLPALPQVVC 20

RESULT 9
US-09-413-564A-18
; Sequence 18, Application US/09413564A
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; APPLICANT: Stevens, Vernon
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564A
; CURRENT FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
US-09-413-564A-18

Query Match 100.0%; Score 86; DB 18; Length 20;
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Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 4 MTRVLQGVLPALPQVVC 20

RESULT 10
US-09-413-564A-38
; Sequence 38, Application US/09413564A
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; APPLICANT: Stevens, Vernon
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564A
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 09/413,564
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
; OTHER INFORMATION: HYDROXYPROLINE AT POSITION 2
US-09-413-564A-38

Query Match 100.0%; Score 86; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 4 MTRVLQGVLPALPQVVC 20

RESULT 11
US-09-413-564A-40
; Sequence 40, Application US/09413564A
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; APPLICANT: Stevens, Vernon
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564A
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
; OTHER INFORMATION: SINGLE SUBSTITUTION AT POSITION 2
US-09-413-564A-40

Query Match 100.0%; Score 86; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 4 MTRVLQGVLPALPQVVC 20

RESULT 12
US-09-413-564C-18
; Sequence 18, Application US/09413564C
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; APPLICANT: Stevens, Vernon
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564C
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
US-09-413-564C-18

Query Match 100.0%; Score 86; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 4 MTRVLQGVLPALPQVVC 20

RESULT 13
US-09-413-564C-38
; Sequence 38, Application US/09413564C
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; APPLICANT: Stevens, Vernon
; TITLE OF INVENTION: Antigenic modification of polypeptides
; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564C
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
; OTHER INFORMATION: HYDROXYPROLINE AT POSITION 2
US-09-413-564C-38

Query Match 100.0%; Score 86; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 4 MTRVLQGVLPALPQVVC 20

RESULT 14
US-09-413-564C-40
; Sequence 40, Application US/09413564C
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; APPLICANT: Stevens, Vernon
; TITLE OF INVENTION: Antigenic modification of polypeptides


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; FILE REFERENCE: URF 2-056 AVI
; CURRENT APPLICATION NUMBER: US/09/413,564C
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 40
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(20)
; OTHER INFORMATION: SINGLE SUBSTITUTION AT POSITION 2
US-09-413-564C-40

Query Match          100.0%; Score 86; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
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Db 4 MTRVLQGVLPALPQVVC 20

RESULT 15
US-09-466-320-6
; Sequence 6, Application US/09466320
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick
; TITLE OF INVENTION: Chorionic Gonadotropin DNA Vaccines and
; FILE REFERENCE: 0450-0026.30
; CURRENT APPLICATION NUMBER: US/09/466,320
; CURRENT FILING DATE: 1999-12-17
; EARLIER APPLICATION NUMBER: US 60/112,910
; EARLIER FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-466-320-6

Query Match          100.0%; Score 86; DB 18; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
   |||||
Db 4 MTRVLQGVLPALPQVVC 20

RESULT 16
US-09-571-497-9
; Sequence 9, Application US/09571497
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Combined Approach to Treatment of Cancer
; FILE REFERENCE: 0450-0027.30
; CURRENT APPLICATION NUMBER: US/09/571,497
; CURRENT FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/134,419
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/134,432
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-571-497-9

Query Match          100.0%; Score 86; DB 23; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
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Db 4 MTRVLQGVLPALPQVVC 20

RESULT 17
US-09-766-397B-6
; Sequence 6, Application US/09766397B
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick
; TITLE OF INVENTION: Chorionic Gonadotropin DNA Vaccines and
; FILE REFERENCE: 0450-0026.31
; CURRENT APPLICATION NUMBER: US/09/766,397B
; CURRENT FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: US 09/466,320
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: US 60/112,910
; PRIOR FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-766-397B-6

Query Match          100.0%; Score 86; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
   |||||
Db 4 MTRVLQGVLPALPQVVC 20

RESULT 18
US-09-915-676-9
; Sequence 9, Application US/09915676
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Combined Approach to Treatment of Cancer
; FILE REFERENCE: 50450-8027.US01
; CURRENT APPLICATION NUMBER: US/09/915,676
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 09/571,497
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/134,419
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/134,432
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-676-9

Query Match          100.0%; Score 86; DB 23; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.9e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Best Local Similarity 100.0%; Pred. No. 3.9e-06; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 4 MTRVLQGVLPALPQVVC 20

RESULT 19
US-09-587-223A-37
; Sequence 37, Application US/09587223A
; GENERAL INFORMATION:
; APPLICANT: Prendergast, Patrick T.
; TITLE OF INVENTION: PEPTIDES FOR THERAPEUTIC USE
; FILE REFERENCE: HOLISED.037A
; CURRENT APPLICATION NUMBER: US/09/587,223A
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 60/137,227
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: IE 2000/0170
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: IE 2000/0303
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: IE 2000/0385
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: IE 2000/0286
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides exhibiting similarity to human clara cell
; OTHER INFORMATION: protein and having immunomodulatory and
; OTHER INFORMATION: therapeutic properties
US-09-587-223A-37

Query Match 100.0%; Score 86; DB 19; Length 24;
Best Local Similarity 100.0%; Pred. No. 4.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 6 MTRVLQGVLPALPQVVC 22

RESULT 20
US-09-587-223A-95
; Sequence 95, Application US/09587223A
; GENERAL INFORMATION:
; APPLICANT: Prendergast, Patrick T.
; TITLE OF INVENTION: PEPTIDES FOR THERAPEUTIC USE
; FILE REFERENCE: HOLISED.037A
; CURRENT APPLICATION NUMBER: US/09/587,223A
; CURRENT FILING DATE: 2000-06-01
; PRIOR APPLICATION NUMBER: 60/137,227
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: IE 2000/0170
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: IE 2000/0303
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: IE 2000/0385
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: IE 2000/0286
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptides exhibiting similarity to human clara cell
; OTHER INFORMATION: protein and having immunomodulatory and
; OTHER INFORMATION: therapeutic properties
US-09-587-223A-95

Query Match 100.0%; Score 86; DB 19; Length 25;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 7 MTRVLQGVLPALPQVVC 23

RESULT 22
PCT-US00-27741-4
; Sequence 4, Application PC/TUS0027741
; GENERAL INFORMATION:
; APPLICANT: The Ohio State University Research Foundation
; TITLE OF INVENTION: Antigenic Modification of Polypeptides
; FILE REFERENCE: URF 2-056 AVPCT
; CURRENT APPLICATION NUMBER: PCT/US00/27741
; CURRENT FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/413,564
; PRIOR FILING DATE: 1999-10-06
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-27741-4
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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:26:40 ; Search time 12.325 Seconds
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84.494 Million cell updates/sec

Title: US-09-821-380-1

Perfect score: 86

Sequence: 1 MTRVLQGLPALPQVVC 17

Scoring table: BLOSUM62

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Searched: 193982 seqs, 61258239 residues

Total number of hits satisfying chosen parameters: 193982

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database :

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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	17	6	US-10-029-206A-44
2	86	100.0	163	5	US-09-724-676-63209
3	86	100.0	163	5	US-09-724-676A-63209
4	86	100.0	165	6	US-10-187-176-7
5	81	94.2	17	6	US-10-029-206A-97
6	80	93.0	17	6	US-10-029-206A-174
7	78	90.7	17	6	US-10-029-206A-99
8	73	84.9	17	6	US-10-029-206A-166
9	72	83.7	15	6	US-10-029-206A-164
10	69	80.2	14	6	US-10-029-206A-171
11	69	80.2	17	6	US-10-029-206A-133
12	69	80.2	127	6	US-10-187-176-8
13	67	77.9	13	6	US-10-029-206A-34
14	67	77.9	15	6	US-10-029-206A-165
15	66	76.7	17	6	US-10-029-206A-139
16	64	74.4	13	6	US-10-029-206A-155
17	57	66.3	15	6	US-10-029-206A-161
18	55	64.0	16	6	US-10-029-206A-100
19	52	60.5	10	6	US-10-029-206A-20
20	50	58.1	10	6	US-10-029-206A-49
21	45	52.3	9	6	US-10-029-206A-157
22	43	50.0	9	6	US-10-029-206A-158
23	42	48.8	9	6	US-10-029-206A-156
24	42	48.8	14	6	US-10-029-206A-106
25	42	48.8	481	5	US-09-724-676-82428
26	42	48.8	481	5	US-09-724-676A-82428

27	41	47.7	8	6	US-10-029-206A-33	Sequence 33, Appl
28	41	47.7	14	6	US-10-029-206A-101	Sequence 101, App
29	41	47.7	745	5	US-09-724-676-71092	Sequence 71092, A
30	41	47.7	745	5	US-09-724-676A-71092	Sequence 71092, A
31	41	47.7	841	6	US-10-198-070-87	Sequence 87, Appl
32	40	46.5	276	5	US-09-724-676-69338	Sequence 69338, A
33	40	46.5	276	5	US-09-724-676-69339	Sequence 69339, A
34	40	46.5	276	5	US-09-724-676A-69338	Sequence 69338, A
35	40	46.5	276	5	US-09-724-676A-69339	Sequence 69339, A
36	40	46.5	319	5	US-09-724-676-69316	Sequence 69316, A
37	40	46.5	319	5	US-09-724-676-69317	Sequence 69317, A
38	40	46.5	319	5	US-09-724-676A-69316	Sequence 69316, A
39	40	46.5	319	5	US-09-724-676A-69317	Sequence 69317, A
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41	40	46.5	378	5	US-09-724-676-69335	Sequence 69335, A
42	40	46.5	378	5	US-09-724-676A-69334	Sequence 69334, A
43	40	46.5	378	5	US-09-724-676A-69335	Sequence 69335, A
44	40	46.5	405	5	US-09-724-676-59936	Sequence 59936, A
45	40	46.5	405	5	US-09-724-676A-59936	Sequence 59936, A
46	40	46.5	415	6	US-10-266-829-101	Sequence 101, App
47	40	46.5	421	5	US-09-724-676-69312	Sequence 69312, A
48	40	46.5	421	5	US-09-724-676-69313	Sequence 69313, A
49	40	46.5	421	5	US-09-724-676A-69312	Sequence 69312, A
50	40	46.5	421	5	US-09-724-676A-69313	Sequence 69313, A
51	40	46.5	665	5	US-09-724-676-69310	Sequence 69310, A
52	40	46.5	665	5	US-09-724-676-69311	Sequence 69311, A
53	40	46.5	665	5	US-09-724-676A-69310	Sequence 69310, A
54	40	46.5	665	5	US-09-724-676A-69311	Sequence 69311, A
55	39	45.3	11	6	US-10-029-206A-103	Sequence 103, App
56	39	45.3	14	6	US-10-029-206A-108	Sequence 108, App
57	39	45.3	65	5	US-09-513-999C-7301	Sequence 7301, App
58	39	45.3	263	1	PCT-US02-32727-21707	Sequence 21707, A
59	39	45.3	364	6	US-10-131-813A-342	Sequence 342, App
60	39	45.3	364	6	US-10-131-813A-342	Sequence 342, App
61	39	45.3	364	6	US-10-131-823A-342	Sequence 342, App
62	39	45.3	364	6	US-10-131-824A-342	Sequence 342, App
63	39	45.3	364	6	US-10-131-826A-342	Sequence 342, App
64	39	45.3	364	6	US-10-131-829A-342	Sequence 342, App
65	39	45.3	364	6	US-10-125-926A-342	Sequence 342, App

ALIGNMENTS

RESULT 1
US-10-029-206A-44
; Sequence 44, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029, 206A
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
; OTHER INFORMATION: signalling molecule
US-10-029-206A-44

Query Match 100.0%; Score 86; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGLPALPQVVC 17
|||||

```
Db      1 MTRVLQGVLPALPQVVC 17

RESULT 2
US-09-724-676-63209
; Sequence 63209, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63209
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-63209

Query Match      100.0%; Score 86; DB 5; Length 163;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTRVLQGVLPALPQVVC 17
        |||||
Db      59 MTRVLQGVLPALPQVVC 75

RESULT 3
US-09-724-676A-63209
; Sequence 63209, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63209
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-63209

Query Match      100.0%; Score 86; DB 5; Length 163;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTRVLQGVLPALPQVVC 17
        |||||
Db      59 MTRVLQGVLPALPQVVC 75

RESULT 4
US-10-187-176-7
; Sequence 7, Application US/10187176
; GENERAL INFORMATION:
; APPLICANT: Ji, Inhae
; APPLICANT: Ji, Inhae
; TITLE OF INVENTION: Agents and Methods for Modulating Interactions Between
; FILE REFERENCE: 028750-221
; CURRENT APPLICATION NUMBER: US/10/187,176
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/301,834
; PRIOR FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 165
; TYPE: PRT

Query Match      93.0%; Score 80; DB 6; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.9e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MTRVLQGVLPALPQVVC 17
        |||||
Db      1 MXRVLQGVLPALPQVVC 17

RESULT 5
US-10-029-206A-174
; Sequence 174, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 174
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NMPP-71
US-10-029-206A-174

Query Match      94.2%; Score 81; DB 6; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.9e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MTRVLQGVLPALPQVVC 17
        |||||
Db      1 MXRVLQGVLPALPQVVC 17

RESULT 6
US-10-029-206A-174
; Sequence 174, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 174
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NMPP-71
US-10-029-206A-174

Query Match      93.0%; Score 80; DB 6; Length 17;
Best Local Similarity 94.1%; Pred. No. 7.9e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MTRVLQGVLPALPQVVC 17
        |||||
Db      1 MXRVLQGVLPALPQVVC 17
```

Best Local Similarity 94.1%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
DB 1 MTRVLPGVLPALPQVVC 17

RESULT 7

US-10-029-206A-99
; Sequence 99, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: A1126906
US-10-029-206A-99

Query Match 90.7%; Score 78; DB 6; Length 17;
Best Local Similarity 82.4%; Pred. No. 2.4e-06;
Matches 14; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
DB 1 ITRVMQGVIPALPQVVC 17

RESULT 8

US-10-029-206A-166
; Sequence 166, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 166
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HLA-DRB1*0301
US-10-029-206A-166

Query Match 84.9%; Score 73; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQV 15
DB 1 MTRVLQGVLPALPQV 15

RESULT 9

US-10-029-206A-164

; Sequence 164, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HLA-DRB1*0101
US-10-029-206A-164

Query Match 83.7%; Score 72; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 TRVLQGVLPALPQV 16
DB 1 TRVLQGVLPALPQV 15

RESULT 10

US-10-029-206A-171
; Sequence 171, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 171
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NMPF-70
US-10-029-206A-171

Query Match 80.2%; Score 69; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQ 14
DB 1 MTRVLQGVLPALPQ 14

RESULT 11

US-10-029-206A-133
; Sequence 133, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380

RESULT 16
US-10-029-206A-155
; Sequence 155, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 155
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SignalP (CBS)
US-10-029-206A-155

Query Match 74.4%; Score 64; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00033;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALP 13
|||||
Db 1 MTRVLQGVLPALP 13

RESULT 17
US-10-029-206A-161
; Sequence 161, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 161
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: MHC II (H2-Ak)
; OTHER INFORMATION: 15-mers
US-10-029-206A-161

Query Match 66.3%; Score 57; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPAL 12
|||||
Db 4 MTRVLQGVLPAL 15

RESULT 18
US-10-029-206A-100
; Sequence 100, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US

; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AT221581
US-10-029-206A-100

Query Match 64.0%; Score 55; DB 6; Length 16;
Best Local Similarity 81.2%; Pred. No. 0.011;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPOVV 16
|||||
Db 1 MTRVLQGVLLALPOLV 16

RESULT 19
US-10-029-206A-20
; Sequence 20, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligopeptide
US-10-029-206A-20

Query Match 60.5%; Score 52; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLPALPOVVC 17
|||||
Db 1 VLPALPOVVC 10

RESULT 20
US-10-029-206A-49
; Sequence 49, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: peptide
; OTHER INFORMATION: signalling molecule
US-10-029-206A-49

Query Match 58.1%; Score 50; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.045;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LGVLPALPQ 14
| | | | | | | |
Db 1 LGVLPALPQ 10

RESULT 21

US-10-029-206A-157
; Sequence 157, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 157
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HLA molecule
; OTHER INFORMATION: type I (A_0201)
US-10-029-206A-157

Query Match 52.3%; Score 45; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GVLPAQV 15
| | | | | | | |
Db 1 GVLPAQV 9

RESULT 22

US-10-029-206A-158
; Sequence 158, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 158
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HLA molecule
; OTHER INFORMATION: type I (A_0201)
US-10-029-206A-158

Query Match 50.0%; Score 43; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 VLPALPQV 16

Db 1 VLPALPQV 9
| | | | | | | |

RESULT 23

US-10-029-206A-156
; Sequence 156, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HLA molecule
; OTHER INFORMATION: type I (A_0201)
US-10-029-206A-156

Query Match 48.8%; Score 42; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLOGVLPAL 12
| | | | | | | |
Db 1 VLOGVLPAL 9

RESULT 24

US-10-029-206A-106
; Sequence 106, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hs.63758.4
US-10-029-206A-106

Query Match 48.8%; Score 42; DB 6; Length 14;
Best Local Similarity 64.3%; Pred. No. 1.2;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 RVLOGVLPALPQV 16
: | | | | | | | |
Db 1 KVLGRLPAVAQV 14

RESULT 25

US-09-724-676-82428
; Sequence 82428, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing

; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724.676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82428
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-82428

Query Match 48.8%; Score 42; DB 5; Length 481;
Best Local Similarity 64.3%; Pred. No. 42;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 RVLQGVLPALPOVV 16
Db 288 KVLQGRLPAAQAV 301

Search completed: December 4, 2002, 11:36:51
Job time : 13.325 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:23:55 ; Search time 15.3 Seconds
(without alignments)
106.816 Million cell updates/sec

Title: US-09-821-380-1
Perfect score: 86
Sequence: 1 MTRVLQGVLPALPOVVC 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : PIR_73:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	145	2	beta-gonadotropin
2	86	100.0	165	1	choriogonadotropin
3	69	80.2	141	1	lutropin beta chain
4	66	76.7	165	1	choriogonadotropin
5	55	64.0	169	1	testicular luteini
6	51	59.3	80	2	testicular luteini
7	51	59.3	119	2	lutropin beta chain
8	51	59.3	138	2	lutropin beta chain
9	51	59.3	141	1	lutropin beta chain
10	51	59.3	141	1	lutropin beta chain
11	51	59.3	141	1	lutropin beta chain
12	50	58.1	139	2	testicular luteini
13	50	58.1	141	1	lutropin beta chain
14	50	58.1	141	1	lutropin beta chain
15	49	57.0	118	2	lutropin beta chain
16	49	57.0	118	2	lutropin beta chain
17	44	51.2	532	2	hypothetical prote
18	43	50.0	304	2	hypothetical prote
19	43	50.0	336	1	BGLF2 protein - hu
20	43	50.0	338	2	hypothetical prote
21	43	50.0	338	2	hypothetical prote
22	43	50.0	2493	2	adenylate cyclase
23	42	48.8	447	2	probable gluconate
24	42	48.8	817	2	hypothetical prote
25	41	47.7	102	2	hypothetical prote
26	41	47.7	206	2	hypothetical prote
27	41	47.7	314	2	hypothetical prote
28	41	47.7	353	2	aspartokinase II a
29	41	47.7	432	2	probable ABC trans

ALIGNMENTS

RESULT 1

I37231

beta-gonadotropin - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jul-2000

C:Accession: I37231

R:Raimadze, K.; Vamvakopoulos, N.C.; Fiddes, J.C.

Nature 307, 37-40, 1984

A:Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin

A:Reference number: I37231; MUID:84093590; PMID:6690982

A:Accession: I37231

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-145 <RES>

A:Cross-references: EMBL:X00266; NID:g29907; PIDN:CAA25069.1; PID:g1335012

C:Genetics:

C:Introns: 41/3

C:Superfamily: pituitary glycoprotein hormone beta chain

Query Match 100.0%; Score 86; DB 2; Length 145;

Best Local Similarity 100.0%; Pred. No. 3.8e-07;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPOVVC 17

|||||

Db 41 MTRVLQGVLPALPOVVC 57

RESULT 2

KTHUB

choriogonadotropin beta chain precursor [validated] - human

N:Alternate names: beta-gonadotropin; chorionic gonadotropin beta chain

C:Species: Homo sapiens (man)
 C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 08-Dec-2000
 C:Accession: A93230; I69972; I55224; I55250; I70007; I70008; A92303; A92181; A92142; PC1
 R:Fiddes, J.C.; Goodman, H.M.
 Nature 286, 684-687, 1980
 A:Title: The cDNA for the beta-subunit of human chorionic gonadotropin suggests evolutionary
 A:Reference number: A93230; MUID:81012134; PMID:6774259
 A:Accession: A93230
 A:Molecule type: mRNA
 A:Residues: 1-165 <PID>
 A:Cross-references: GB:J00117; GB:M38559; GB:M54963; NID:gl180436; PIDN:AAA96690.1; PID:9
 J.Policastro, P.; Ovit, C.E.; Hoshina, M.; Fukuoaka, H.; Boothby, M.R.; Boime, I.
 J. Biol. Chem. 258, 11492-11499, 1983
 A:Title: The beta subunit of human chorionic gonadotropin is encoded by multiple genes.
 A:Reference number: I55224; MUID:84008141; PMID:6194155
 A:Accession: I69972
 A:Molecule type: mRNA
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-165 <POL>
 A:Cross-references: GB:K03189; NID:gl180450; PIDN:AAA53288.1; PID:gl180453
 A:Note: clone CG-beta-e
 A:Accession: I55224
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-23, 'W', 25-136, 'A', 138-165 <PO2>
 A:Cross-references: GB:K03183; NID:gl180442; PIDN:AAA53287.1; PID:gl180444
 A:Note: clone CG-beta-a
 J.Policastro, P.F.; Daniels-McQueen, S.; Carle, G.; Boime, I.
 J. Biol. Chem. 261, 5907-5916, 1986
 A:Title: A map of the hCG beta-LH beta gene cluster.
 A:Reference number: I55250; MUID:86195987; PMID:2422163
 A:Accession: I55250
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5 <PO3>
 A:Cross-references: GB:M13504; NID:gl180419; PIDN:AAA52005.1; PID:g463088
 A:Note: CG-beta-3 gene
 A:Accession: I70007
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5 <PO4>
 A:Cross-references: GB:M13505; NID:gl180429; PIDN:AAA52008.1; PID:g463089
 A:Note: CG-beta-6 gene
 A:Accession: I70008
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-5 <RE5>
 A:Cross-references: GB:M13503; NID:gl180432; PIDN:AAA52009.1; PID:g463090
 A:Note: CG-beta-7 gene
 R.Birken, S.; Fetherston, J.; Canfield, R.; Boime, I.
 J. Biol. Chem. 256, 1816-1823, 1981
 A:Title: The amino acid sequences of the prepeptides contained in the alpha and beta sub
 A:Reference number: A92303; MUID:81117268; PMID:7462224
 A:Accession: A92303
 A:Molecule type: protein
 A:Residues: 1-20 <BI>
 A:Note: the identity of the residue at position 19 could not be determined
 R.Morgan, F.J.; Birken, S.; Canfield, R.E.
 J. Biol. Chem. 250, 5247-5258, 1975
 A:Title: The amino acid sequence of human chorionic gonadotropin. The alpha subunit and
 A:Reference number: A92181; MUID:75211304; PMID:1150658
 A:Accession: A92181
 A:Molecule type: protein
 A:Residues: 21-165 <MOR>
 R.Carlsen, R.B.; Bahl, O.P.; Swaminathan, N.
 J. Biol. Chem. 248, 6810-6827, 1973
 A:Reference number: A92142; MUID:74011267; PMID:4795659
 A:Accession: A92142
 A:Molecule type: protein
 A:Residues: 21-22, 'Q', 24-73, 'ZL', 76-140, 142-157, 'PB', 160-165, 'SLP' <CAR>
 R.Shi, Z.P.; Lu, G.G.; Li, W.X.; Liu, X.J.; Li, S.Z.; Xu, Y.S.; Wang, Y.
 Chinese Biochem. J. 6, 558-562, 1990
 A:Title: The immunological characteristics of the enzymatic fragments of human chorionid

A:Reference number: PC1016
 A:Accession: PC1016
 A:Molecule type: protein
 A:Residues: 21-165 <SHD>
 A:Note: article in Chinese with English abstract
 R.Birken, S.; Armstrong, E.G.; Kolks, M.A.G.; Cole, L.A.; Agosto, G.M.; Krichevsky, A
 Endocrinology 123, 572-583, 1988
 A:Title: Structure of the human chorionic gonadotropin beta-subunit fragment from pre
 A:Reference number: A61097; MUID:88254680; PMID:2454811
 A:Accession: A61097
 A:Molecule type: protein
 A:Residues: 26-32, 'X', 34-49, 'X', 51-60; 75-112 <BI2>
 A:Note: this material from pregnancy urine lacks sialic acid in its carbohydrate and h
 R.Kardana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.
 Br. J. Cancer 67, 686-692, 1993
 A:Title: Characterisation of UGP and its relationship with beta-core fragment.
 A:Reference number: A56873; MUID:93229246; PMID:8471426
 A:Accession: B56873
 A:Molecule type: protein
 A:Residues: 26-28, 'X', 30-32, 'X', 34-42, 'X', 44-45, 'X', 47-48; 75-76, 'X', 78-91, 'G', 93-102
 A:Experimental source: urine
 A:Note: sequence modified after extraction from NCBI backbone
 A:Note: this material was designated urinary gonadotropin peptide (peak 2)
 R.Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader, J.W.; Canfield, R.E.; Mach
 Nature 369, 455-461, 1994
 A:Title: Crystal structure of human chorionic gonadotropin.
 A:Reference number: A44674; MUID:94261179; PMID:8202136
 A:Contents: annotation: X-ray crystallography, 3.0 angstroms; correction of disulfide
 R.Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
 Nature 307, 37-40, 1984
 A:Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin
 A:Reference number: I37231; MUID:84093590; PMID:6690982
 A:Accession: I37412
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 21-165 <RES>
 A:Cross-references: EMBL:X00265; NID:g31719; PIDN:CAA25068.1; PID:gl1335075
 C:Genetics:
 A:Gene: GDB:GDB
 A:Cross-references: GDB:119055; OMIM:118860
 A:Map position: 19q13.3-19q13.3
 A:Introns: 5/3; 61/3
 A:Note: the chorionadotropin beta chain locus contains six genes (or pseudogenes)
 C:Superfamily: pituitary glycoprotein hormone beta chain
 C:Keywords: glycoprotein; hormone; pituitary
 F:1-20/Domain: signal sequence #status experimental <SIG>
 F:21-165/Product: chorionadotropin beta chain #status experimental <MAT>
 F:29-77, 43-92, 46-130, 54-108, 58-110, 113-120/Disulfide bonds: #status experimental
 F:33,50/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:138,150/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:141,147,152,158/Binding site: carbohydrate (Ser) (covalent) #status experimental
 Query Match 100.0%; Score 86; DB 1; Length 165;
 Best Local Similarity 100.0%; Pred. No. 4.4e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTRVLQGLPALPQVVC 17
 Db 61 MTRVLQGLPALPQVVC 77
 |||||
 RESULT 3
 UTHUB
 lutropin beta chain precursor [validated] - human
 N:Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing
 C:Species: Homo sapiens (man)
 C:Date: 13-Jul-1981 #sequence_revision 24-Nov-1999 #text_change 20-Apr-2001
 C:Accession: I37994; I58013; A90604; A92759; A94466; A01497; B94552
 R.Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
 Nature 307, 37-40, 1984
 A:Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin
 A:Reference number: I37231; MUID:84093590; PMID:6690982
 A:Accession: I37994

A:Status: preliminary; translated from GB/EMBL/DBJ; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-141 <FAL>
A:Cross-references: GB:X00264; NID:G34351; PIDN:CAA25067.1; PID:g2292893
R:Weiss, J.; Axelrod, L.; Whitcomb, R.W.; Harris, P.E.; Crowley, W.F.; Jameson, J.L.
N. Engl. J. Med. 326, 179-183, 1992
A:Title: Hypogonadism caused by a single amino acid substitution in the beta subunit of
A:Reference number: I58013; MUID:92085985; PMID:1727547
A:Accession: I58013
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 72-73, 'R', 75-76 <WEI>
A:Cross-references: GB:S71273; NID:Q240572; PIDN:AAI14960.1; PID:g4262812
A:Note: mutant sequence from patient with hypogonadism
R:Sairam, M.R.; Li, C.H.
Biochim. Biophys. Acta 412, 70-81, 1975
A:Title: Human pituitary lutropin. Isolation, properties, and the complete amino acid se
A:Reference number: A90604; MUID:76062547; PMID:1191677
A:Accession: A90604
A:Molecule type: protein
A:Residues: 21-38, 'Q', 40-75, 77-131, 133-134, 'H', 136-137 <SAI>
R:Shome, B.; Parlow, A.F.
J. Clin. Endocrinol. Metab. 36, 618-621, 1973
A:Title: The primary structure of the hormone-specific, beta subunit of human pituitary
A:Reference number: A92759; MUID:73090987; PMID:4685398
A:Accession: A92759
A:Molecule type: protein
A:Residues: 21-38, 'Q', 40-75, 77-131, 133-134, 'H', 136-137 <SHO>
R:Closset, J.; Hennen, G.; Lequin, R.M.
FEBS Lett. 29, 97-100, 1973
A:Title: Human luteinizing hormone the amino acid sequence of the beta subunit.
A:Reference number: A91389; MUID:73221227; PMID:4719207
A:Contents: annotation; partial sequence
R:Ward, D.N.
unpublished results, cited by Closset, J., Hennen, G., and Lequin, R.M., FEBS Lett. 29,
A:Reference number: A94466
A:Accession: A94466
A:Molecule type: protein
A:Residues: 21-38, 'Q', 40-46 <WAR>
A:Note: 28-Val, 33-Arg, and 35-Thr were also found
R:Shome, B.; Parlow, A.F.
submitted to the Atlas, April 1975
A:Reference number: A94552
A:Contents: annotation; binding site
C:Genetics:
A:Gene: GDB:LHB
A:Cross-references: GDB:119364; OMIM:152780
A:Map position: 19q13.3-19q13.3
C:Superfamily: pituitary glycoprotein hormone beta chain
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-141/Product: lutropin beta #status experimental <LUTB>
F:21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #stat
F:29-54, 43-77, 46-108, 58-130, 92-120, 110-113/Disulfide bonds: #status predicted
F:50/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 80.2%; Score 69; DB 1; Length 141;
Best Local Similarity 82.4%; Pred. No. 0.00027;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 61 MMRVLQAVLPPLPQVVC 77

RESULT 4
KTBA
Choriongonadotropin beta chain precursor - olive baboon
C:Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 28-May-1999
C:Accession: A25808
R:Crawford, R.J.; Tregear, G.W.; Niall, H.D.
Gene 46, 161-169, 1986

A:Title: The nucleotide sequences of baboon chorionic gonadotropin beta-subunit genes
A:Reference number: A25808; MUID:87108851; PMID:2433190
A:Accession: A25808
A:Molecule type: mRNA
A:Residues: 1-165 <CRA>
A:Cross-references: GB:M14966; NID:g176572; PIDN:AAA35383.1; PID:g176573
C:Comment: There are at least five copies of CG-related genes and at least two of the
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; hormone; placenta; pregnancy maintenance
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-165/Product: choriongonadotropin beta chain #status predicted <CGB>
F:29-77, 43-92, 46-130, 58-110, 113-120/Disulfide bonds: #status predicted
F:33, 50/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:140, 147, 152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 76.7%; Score 66; DB 1; Length 165;
Best Local Similarity 76.5%; Pred. No. 0.001;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 61 MMRVLQAVLPPLPQVVC 77

RESULT 5
KTHOB
Choriongonadotropin beta chain precursor - horse
N:Alternate names: chorionic gonadotropin beta chain (CG); luteinizing hormone (LH) b
C:Species: Equus caballus (domestic horse)
C>Date: 14-Nov-1983 #sequence_revision 03-May-1996 #text_change 18-Jun-1999
C:Accession: A41917; A29304; A29305; A01503
R:Sherman, G.B.; Wolfe, M.W.; Farmerie, T.A.; Clay, C.M.; Threadgill, D.S.; Sharp, D.
Mol. Endocrinol. 6, 951-959, 1992
A:Title: A single gene encodes the beta-subunits of equine luteinizing hormone and ch
A:Reference number: A41917; MUID:92357035; PMID:1379674
A:Accession: A41917
A:Molecule type: DNA
A:Residues: 1-169 <SHE>
A:Cross-references: GB:S41704; NID:g252740; PIDN:AAB22775.1; PID:g252741
A:Experimental source: sperm
A:Note: sequence extracted from NCBI backbone (NCBIN:110184, NCBIP:110185)
R:Sugino, H.; Bousfield, G.R.; Moore Jr., W.T.; Ward, D.N.
J. Biol. Chem. 262, 8603-8609, 1987
A:Title: Structural studies on equine glycoprotein hormones. Amino acid sequence of e
A:Reference number: A29304; MUID:87250475; PMID:3298238
A:Accession: A29304
A:Molecule type: protein
A:Residues: 21-169 <SUG>
R:Bousfield, G.R.; Liu, W.K.; Sugino, H.; Ward, D.N.
J. Biol. Chem. 262, 8610-8620, 1987
A:Title: Structural studies on equine glycoprotein hormones. Amino acid sequence of e
A:Reference number: A29305; MUID:87250476; PMID:3298239
A:Accession: A29305
A:Molecule type: protein
A:Residues: 21-169 <BOU>
R:Ward, D.N.; Moore Jr., W.T.; Burleigh, B.D.
J. Protein Chem. 1, 263-280, 1982
A:Title: Structural studies on equine chorionic gonadotropin.
A:Reference number: A01503
A:Accession: A01503
A:Molecule type: protein
A:Residues: 21-40, 'Q', 42-43, 'SK', 46, 'XXX', 51, 'T', 53-64, 'T', 66-96, 'B', 98, 'R', 100-102,
R:Matsui, T.; Mizuochi, T.; Titani, K.; Okinaga, T.; Hoshi, M.; Bousfield, G.R.; Sug
Biochemistry 33, 14039-14048, 1994
A:Title: Structural analysis of N-linked oligosaccharides of equine chorionic gonadot
A:Reference number: A59552; MUID:95034847; PMID:7524670
A:Contents: annotation; glycosylation
A:Note: horse lutropin and choriongonadotropin beta chains have identical protein chai
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; hormone; pituitary
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-169/Product: choriongonadotropin beta chain #status experimental <MAT>
F:29-77, 43-92, 46-130, 54-108, 58-110, 113-120/Disulfide bonds: #status predicted

F:33/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 64.08; Score 55; DB 1; Length 169;
Best Local Similarity 58.8%; Pred. No. 0.076;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17

Db 61 MVRVMPALPALPQVVC 77

RESULT 6

I65235
testicular luteinizing hormone beta subunit - rat
C:Species: Rattus norvegicus (Norway Rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C:Accession: I65235
R:Zhang, F.P.; Rannikko, A.; Huhtaniemi, I.
Biochem. Biophys. Res. Commun. 210, 858-865, 1995
A:Title: Isolation and characterization of testis-specific cDNAs for luteinizing hormone
A:Reference number: I52320; MUID:95283549; PMID:7763258
A:Accession: I65235
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-80 <RES>
A:Cross-references: EMBL:U25803; NID:g904025; PIDN:AAC52251.1; PID:g904026
C:Genetics:
A:Gene: TLHB3
C:Superfamily: pituitary glycoprotein hormone beta chain

Query Match 59.3%; Score 51; DB 2; Length 80;

Best Local Similarity 58.8%; Pred. No. 0.17;

Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17

Db 1 MVRVLPALPPVPQVVC 17

RESULT 7

A61465
lutropin beta chain - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 08-Dec-1995
C:Accession: A61465
R:Glenn, S.D.; Nahm, H.S.; Ward, D.N.
J. Protein Chem. 3, 259-273, 1984
A:Title: The amino acid sequence of the rabbit lutropin beta subunit.
A:Reference number: A61465
A:Accession: A61465
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-119 <GLE>
A:Note: the sequence from Fig. 1 is inconsistent with that from the abstract in having 1
C:Superfamily: pituitary glycoprotein hormone beta chain
F:11-36,25-59,28-90,40-112,74-102,92-95/Disulfide bonds: #status predicted

Query Match 59.3%; Score 51; DB 2; Length 119;

Best Local Similarity 58.8%; Pred. No. 0.25;

Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17

Db 43 MVRVLPALPPVPQVVC 59

RESULT 8

S00512
lutropin beta chain precursor - dog (fragment)
N:Alternate names: luteinizing hormone beta chain
C:Species: Canis lupus familiaris (dog)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C:Accession: S00512

Query Match 59.3%; Score 51; DB 2; Length 119;

Best Local Similarity 58.8%; Pred. No. 0.25;

Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17

Db 43 MVRVLPALPPVPQVVC 59

RESULT 9

U0018
lutropin beta chain precursor - rat
N:Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing hormone (LH) beta chain
C:Species: Rattus norvegicus (Norway Rat)
C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 24-Sep-1999
C:Accession: A01498; PQ0091; S42527; I83049
R:Jameson, L.; Chin, W.W.; Hollenberg, A.N.; Chang, A.S.; Habener, J.F.
J. Biol. Chem. 259, 15474-15480, 1984
A:Title: The gene encoding the beta-subunit of rat luteinizing hormone. Analysis of ge
A:Reference number: A01498; MUID:85080043; PMID:6096374
A:Accession: A01498
A:Molecule type: DNA
A:Residues: 1-141 <JAM>
A:Cross-references: EMBL:J00749; NID:g205175; PIDN:AAA96703.1; PID:g205176
R:Kato, Y.; Ezashi, T.; Hirai, T.; Kato, T.
Submitted to JIPID, July 1990
A:Reference number: PQ0091
A:Accession: PQ0091
A:Molecule type: mRNA
A:Residues: 4-141 <KAT>
R:Chin, W.W.; Godine, J.E.; Klein, D.R.; Chang, A.S.; Tan, L.K.; Habener, J.F.
Proc. Natl. Acad. Sci. U.S.A. 80, 4649-4653, 1983
A:Title: Nucleotide sequence of the cDNA encoding the precursor of the beta subunit o
A:Reference number: S42527; MUID:83273673; PMID:6192440
A:Accession: S42527
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-141 <CHI>
R:Kato, Y.; Ezashi, T.; Hirai, T.; Kato, T.
Zool. Sci. 7, 879-887, 1990
A:Title: Strain Difference in Nucleotide Sequences of Rat Glycoprotein Hormone Subunit
A:Reference number: I60104
A:Accession: I83049
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 4-141 <RES>
A:Cross-references: GB:D00576; NID:g220807; PIDN:BAA00454.1; PID:g220808
C:Comment: The beta chain confers the specificity of the hormone.
C:Genetics:
A:Introns: 5/3; 61/3
C:Superfamily: pituitary glycoprotein hormone beta chain
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-141/Product: lutropin beta #status predicted <LNB>
F:29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F:33/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 59.3%; Score 51; DB 1; Length 141;

Best Local Similarity 58.8%; Pred. No. 0.3;

R:Wolf, D.L.; Appleby, V.L.; Hjerrild, K.; Baker, A.R.; Talmadge, K.
Nucleic Acids Res. 15, 10602, 1987
A:Title: Nucleic acid and amino acid sequences of dog beta-LH: comparison to rat, cow
A:Reference number: S00512; MUID:88096605; PMID:3697104
A:Accession: S00512
A:Molecule type: mRNA
A:Residues: 1-138 <WOL>
A:Cross-references: EMBL:Y00518; NID:g907; PIDN:CAA68572.1; PID:g860906
C:Superfamily: pituitary glycoprotein hormone beta chain
F:1-17/Domain: signal sequence (fragment) #status predicted <SIG>
F:18-138/Product: lutropin beta chain #status predicted <MAT>
F:26-51,40-74,43-105,55-127,89-117,107-110/Disulfide bonds: #status predicted

Query Match 59.3%; Score 51; DB 2; Length 138;

Best Local Similarity 58.8%; Pred. No. 0.29;

Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17

Db 58 MVRVLPALPPVPQVVC 74

A:Reference number: A92518; MUID:85182575; PMID:3838746
A:Accession: A92518
A:Molecule type: mRNA
A:Residues: 3-111,'S',113-141 <MAU>
A:Cross-references: GB:M10077; NID:g163300; PIDN:AAA30623.1; PID:g163301
R:Maghuin-Rogister, G.; Hennen, G.
Eur. J. Biochem. 39, 235-253, 1973
A:Title: Luteinizing hormone. The primary structures of the beta-subunit from bovine and human.
A:Reference number: A91212; MUID:74075724; PMID:4770795
A:Accession: A91212
A:Molecule type: protein
A:Residues: 21-73,'E',75-121,'PG',124-125,'E',127-139 <MAG>
A:Note: some carboxyl-terminal heterogeneity was found
C:Genetics:
A:Introns: 5/3; 61/3
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: blocked amino end; glycoprotein; hormone; pituitary
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-141/Product: lutropin beta #status experimental <LTB>
F:21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #status predicted
F:29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F:33/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 58.1%; Score 50; DB 1; Length 141;
Best Local Similarity 58.8%; Pred. No. 0.44;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
| | | | : | | : | | |
Db 61 MKRVLVILPPMPQVVC 77

RESULT 14
UTSHB
lutropin beta chain precursor - sheep
N:Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing hormone
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 24-Apr-1984 #sequence_revision 19-Jan-2001 #text_change 19-Jan-2001
C:Accession: I46949; S09232; A92110; A90053; B61098; A01500
R:Brown, P.; McNeill, J.R.; Wallace, R.M.; McNelly, A.S.; Clark, A.J.
Mol. Cell. Endocrinol. 93, 157-165, 1993
A:Title: Characterization of the ovine LH beta-subunit gene: the promoter directs gonadal expression
A:Reference number: I46949; MUID:93351742; PMID:8349025
A:Accession: I46949
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-141 <BRO>
A:Cross-references: GB:S64695; NID:g408240; PIDN:AAB27819.1; PID:g408241
R:d'Angelo-Bernard, G.; Moumni, M.; Jutisz, M.; Counis, R.
Nucleic Acids Res. 18, 2175, 1990
A:Title: Cloning and sequence analysis of the cDNA for the precursor of the beta subunit of ovine luteinizing hormone
A:Reference number: S09232; MUID:90245669; PMID:2336396
A:Accession: S09232
A:Molecule type: mRNA
A:Residues: 1-58,'L',60-62,'Q',64-141 <ANG>
A:Cross-references: EMBL:X52488; NID:g1319; PIDN:CAA36729.1; PID:g1320
R:Liu, W.K.; Nahm, H.S.; Sweeney, C.M.; Holcomb, G.N.; Ward, D.N.
J. Biol. Chem. 247, 4365-4381, 1972
A:Title: The primary structure of ovine luteinizing hormone. II. The amino acid sequence of the primary structure of ovine luteinizing hormone
A:Reference number: A92110; MUID:72211145; PMID:4556309
A:Accession: A92110
A:Molecule type: protein
A:Residues: 21-121,'PG',124-125,'E',127-139 <LIU>
R:Sairam, M.R.; Sany, T.S.A.; Pakkoff, H.; Li, C.H.
Arch. Biochem. Biophys. 153, 572-586, 1972
A:Title: The primary structure of ovine interstitial cell-stimulating hormone. II. The amino acid sequence of the primary structure of ovine interstitial cell-stimulating hormone
A:Reference number: A90053; MUID:73190035; PMID:4575435
A:Accession: A90053
A:Molecule type: protein
A:Residues: 21-29,'E',31-71,'P',72-80,'Q',82-121,'PG',124-125,'E',127-139 <SAI>
R:Nomura, K.; Tsunasawa, S.; Ohmura, K.; Sakayama, F.; Shizume, K.
Endocrinology 123, 700-712, 1988
A:Title: Renotropic activity in ovine luteinizing hormone isoform(s).

A:Reference number: A61098; MUID:88283534; PMID:2456202
A:Accession: B61098
A:Molecule type: protein
A:Residues: 21-39,'N',41-49,64-78,'V',80-82,84-106,115-121,'PG',124-138 <NOM>
A:Note: this form was designated form beta-3; forms beta-1 and beta-2 each lack several amino acids
C:Genetics:
A:Introns: 5/3; 61/3
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: blocked amino end; glycoprotein; hormone; pituitary
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-141/Product: lutropin beta chain #status experimental <MAT>
F:21/Modified site: blocked amino end (Ser) (in mature form) (partial) (probably acet
F:29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F:33/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 58.1%; Score 50; DB 1; Length 141;
Best Local Similarity 58.8%; Pred. No. 0.44;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
| | | | : | | : | | |
Db 61 MKRVLVILPPMPQVVC 77

RESULT 15
PN0141
lutropin beta chain - sperm whale
N:Alternate names: luteinizing hormone beta chain
C:Species: Physeter catodon (sperm whale)
C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 07-May-1993
C:Accession: PN0141
R:Pankov, Y.A.; Karasev, V.S.
Biochimia 49, 1004-1018, 1984
A:Title: Luteinizing hormone of the sperm-whale: amino acid sequence of reduced and native forms
A:Reference number: PN0141; MUID:84281133; PMID:6466737
A:Accession: PN0141
A:Molecule type: protein
A:Residues: 1-118 <PAN>
A:Note: article in Russian with English abstract
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; hormone
F:9-34,23-57,26-88,38-110,72-100,90-93/Disulfide bonds: #status predicted
F:13/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 57.0%; Score 49; DB 2; Length 118;
Best Local Similarity 52.9%; Pred. No. 0.54;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
| | | | : | | : | | |
Db 41 MVRVLPALPPVZPVC 57

RESULT 16
PN0139
lutropin beta chain - minke whale
N:Alternate names: luteinizing hormone beta chain
C:Species: Balaeoptera acutorostrata (minke whale, lesser rorqual)
C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 08-Dec-1995
C:Accession: PN0139
R:Karasev, V.S.; Pankov, Y.A.
Biochimia 50, 1972-1986, 1985
A:Title: Amino acid sequence of reduced and carboxymethylated alpha- and beta-subunit
A:Reference number: PN0138
A:Accession: PN0139
A:Molecule type: protein
A:Residues: 1-118 <RAR>
A:Note: article in Russian with English abstract
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; hormone
F:9-34,23-57,26-88,38-110,72-100,90-93/Disulfide bonds: #status predicted
F:13/Binding site: carbohydrate (Asn) (covalent) #status experimental

ster, E.W.
 A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AD3052
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-338 <KUR>
 A:Cross-references: GB:AE008689; PIDN:AAL44834.1; PID:g17742478; GSPDB:GN00187
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu4033
 A:Map position: linear chromosome

Query Match 50.0%; Score 43; DB 2; Length 338;
 Best Local Similarity 53.8%; Pred. No. 16;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 RVLGVLPAPOV 15
 | : ||| : || :
 DB 204 RAVAGILPSLPEV 216

RESULT 22

A5481
 adenylate cyclase (EC 4.6.1.1) uac1 - smut fungus (*Ustilago maydis*)

C:Species: *Ustilago maydis* (corn smut)
 C:Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 21-Jul-2000
 C:Accession: A55481
 R:Gold, S.; Duncan, G.; Barrett, K.; Kronstad, J.
 Genes Dev. 8, 2805-2816, 1994
 A:Title: cAMP regulates morphogenesis in the fungal pathogen *Ustilago maydis*.
 A:Reference number: A55481; PMID:95087882; PMID:7995519
 A:Accession: A55481
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-2493 <GOL>

A:Cross-references: GB:L33918; NID:g603939; PIDN:AAA57469.1; PID:g603940
 A:Note: nucleotide sequence not given; amino acid sequence not complete
 C:Genetics:
 A:Superfamily: uac1
 C:Keywords: phosphorus-oxygen lyase

C:Superfamily: yeast adenylate cyclase catalytic domain homology; leucine-rich alpha-2-glycoprotein
 F:1181-1203/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR1>
 F:1227-1249/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR2>
 F:1250-1272/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR3>
 F:1363-1382/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR4>
 F:1386-1408/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR5>
 F:1409-1431/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR6>
 F:1535-1558/Domain: leucine-rich alpha-2-glycoprotein repeat homology <LRR7>
 F:2054-2138/Domain: yeast adenylate cyclase catalytic domain homology <YACC>

Query Match 50.0%; Score 43; DB 2; Length 2493;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPOV 16
 ||| : || : || :
 DB 1350 MTRLEGLFPQLPALV 1365

RESULT 23

AE0094

probable gluconate transporter gntP [imported] - *Yersinia pestis* (strain CO92)

C:Species: *Yersinia pestis*
 C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
 C:Accession: AE0094
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell, Nature 413, 523-527, 2001

A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
 A:Reference number: AB0001; PMID:21470413; PMID:11586360

A:Accession: AE0094
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-447 <KUR>
 A:Cross-references: GB:AL590842; PIDN:CAC89616.1; PID:g15978845; GSPDB:GN00175
 C:Genetics:
 A:Gene: gntP
 C:Superfamily: D-serine permease

Query Match 48.8%; Score 42; DB 2; Length 447;
 Best Local Similarity 53.8%; Pred. No. 32;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 LOGVLPALPOVVC 17
 : ||| ||| : || :
 DB 179 IYGLVAIPSVIC 191

RESULT 24

TL6409

hypothetical protein F48E8.6 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: TL6409
 R:Kirsten, J.
 submitted to the EMBL Data Library, March 1995
 A:Description: The sequence of *C. elegans* cosmid F48E8.
 A:Reference number: S59413
 A:Accession: TL6409
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-817 <KIR>
 A:Cross-references: EMBL:U23514; NID:g746484; PID:g746490; PIDN:AAC46543.1; CESP:F48E
 A:Experimental source: strain Bristol N2
 C:Genetics:
 A:Gene: CESP:F48E8.6
 A:Introns: 107/3; 510/3; 670/3; 733/3

Query Match 48.8%; Score 42; DB 2; Length 817;
 Best Local Similarity 43.8%; Pred. No. 60;
 Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 TRVLQGVLPALPOVVC 17
 : : ||| : ||| :
 DB 371 TYLSQTVIPMLPILC 386

RESULT 25

T23320

hypothetical protein K04G11.6 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
 C:Accession: T23320; T26015

submitted to the EMBL Data Library, August 1996

A:Reference number: Z19726

A:Accession: T23320

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-102 <WIL>

A:Cross-references: EMBL:Z78544; PIDN:CAB01763.1; GSPDB:GN00028; CESP:K04G11.6

A:Experimental source: clone K04G11

R:Smyle, R.

submitted to the EMBL Data Library, August 1998

A:Reference number: Z20132

A:Accession: T26015

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-102 <W12>

A:Cross-references: EMBL:AL031265; PIDN:CAA20328.1; GSPDB:GN00028; CESP:K04G11.6

A:Experimental source: clone VK04G11

C:Genetics:

A:Gene: CESP:K04G11.6

A:Map position: X
A:Introns: 43/2
C:Superfamily: Caenorhabditis elegans hypothetical protein K04G11.6

Query Match 47.7%; Score 41; DB 2; Length 102;
Best Local Similarity 63.6%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GVLPALPQVVC 17
I:| | | | |
Db 71 GILPNLPQNLC 81

Search completed: December 4, 2002, 11:27:15
Job time : 17.3 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:23:34 ; Search time 8.5 Seconds
(without alignments)
82.953 Million cell updates/sec

Title: US-09-821-380-1
Perfect score: 86
Sequence: 1 MTRVLQGVLPALPQVVC 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	165	1 CGHB_HUMAN	P01233 homo sapien
2	69	80.2	141	1 LSHB_HUMAN	P01229 homo sapien
3	66	76.7	165	1 CGHB_PAPAN	P07434 papio anubi
4	61	70.9	164	1 CGHB_CALJA	P51500 callithrix
5	55	64.0	169	1 LSHB_HORSE	P08751 equus caball
6	51	59.3	128	1 LSHB_PHOSU	Q9gya9 phodopus su
7	51	59.3	138	1 LSHB_CANFA	P18842 canis fami
8	51	59.3	138	1 LSHB_MACRU	O46483 macropus ru
9	51	59.3	141	1 LSHB_MOUSE	O09108 mus musculu
10	51	59.3	141	1 LSHB_PIG	P01232 sus scrofa
11	51	59.3	141	1 LSHB_RAT	P01230 rattus norv
12	50	58.1	141	1 LSHB_BOVIN	P04651 bos taurus
13	50	58.1	141	1 LSHB_SHEEP	P01231 ovis aries
14	50	58.1	143	1 LSHB_FELCA	O77805 felis silve
15	50	58.1	169	1 LSHB_EQUAS	P19794 equus asinu
16	50	58.1	169	1 LSHB_EQUBU	O46641 equus burch
17	49	57.0	118	1 LSHB_BALAC	P33088 balaeonopte
18	49	57.0	118	1 LSHB_PHYCA	P25330 physeter ca
19	49	57.0	141	1 LSHB_CERSI	O77835 ceratotheri
20	49	57.0	141	1 LSHB_TRIVU	O46482 trichosurus
21	43	50.0	336	1 UL16_EBV	P03221 Epstein-bar
22	43	50.0	1818	1 LSHB_HUMAN	O94822 homo sapien
23	43	50.0	2493	1 CVAAL_USTWA	P49606 ustilago ma
24	43	50.0	2564	1 SPQC_HUMAN	Q9h254 homo sapien
25	42	48.8	801	1 TFR2_HUMAN	Q9p525 homo sapien
26	42	48.8	817	1 YR86_CAEEL	Q9p568 caenorhabdi
27	41	47.7	622	1 PPCC_MOUSE	Q9z2v4 mus musculu
28	41	47.7	841	1 NEK4_HUMAN	P51957 homo sapien
29	40	46.5	383	1 TGT_RALSO	Q8xv44 talstonia s
30	40	46.5	521	1 GAG_HV2D2	P15832 human immun
31	40	46.5	622	1 PPCC_HUMAN	P35558 homo sapien
32	39	45.3	364	1 GDF3_HUMAN	Q9nr23 homo sapien
33	39	45.3	376	1 TGT_CLOAB	Q97gt3 clostridium

34	39	45.3	386	1	DCUP_DROVI	O18601 drosophila
35	39	45.3	463	1	ENGA_MYCTU	O33212 mycobacteri
36	39	45.3	554	1	GYRA_MYCFV	Q49166 mycobacteri
37	39	45.3	622	1	PFCC_RAT	P07379 rattus norv
38	39	45.3	676	1	CMF_RHIME	P45404 rhizobium m
39	38.5	44.8	540	1	C314_DROME	Q9vuf8 drosophila
40	38	44.2	155	1	DUT_GAUCR	Q9a253 caulobacter
41	38	44.2	347	1	NUSA_MYCLE	Q9z5j1 mycobacteri
42	38	44.2	373	1	CCR2_MOUSE	P51683 mus musculu
43	38	44.2	373	1	CCR2_RAT	O55193 rattus norv
44	38	44.2	430	1	AROA_LACLA	Q9ceu0 lactococcus
45	38	44.2	430	1	AROA_LACLC	P43905 lactococcus
46	38	44.2	430	1	GNTF_ECOLI	P39373 escherichia
47	38	44.2	453	1	PABB_ECOLI	P05041 escherichia
48	38	44.2	486	1	SUCP_STRMD	P10249 streptococc
49	38	44.2	493	1	VL2_PAPVD	P03110 deer papill
50	38	44.2	646	1	WEEL_HUMAN	P30291 homo sapien
51	38	44.2	646	1	WEEL_MOUSE	P47810 mus musculu
52	38	44.2	646	1	WEEL_RAT	Q63802 rattus norv
53	38	44.2	682	1	SNK_MOUSE	P53351 mus musculu
54	38	44.2	682	1	SNK_RAT	Q9r012 rattus norv
55	38	44.2	685	1	SNK_HUMAN	Q9nyv3 homo sapien
56	38	44.2	865	1	ENV_SIVAT	P05886 simian immu
57	38	44.2	890	1	IMB2_HUMAN	Q92973 homo sapien
58	38	44.2	1336	1	MAM1_SCHPO	P78966 schizosacch
59	37.5	43.6	1094	1	YB00_YEAST	P38114 saccharomyc
60	37	43.0	121	1	VOR4_P1AMV	Q07520 plantago as
61	37	43.0	325	1	RCEM_CHRVI	P51763 chromatium
62	37	43.0	328	1	MRAW_NEIMA	Q9jys9 neisseria m
63	37	43.0	328	1	MRAW_NEIMB	Q9k020 neisseria m
64	37	43.0	338	1	RTCA_ECOLI	P46849 escherichia
65	37	43.0	342	1	RTCA_ECO57	P58127 escherichia

ALIGNMENTS

RESULT 1	CGHB_HUMAN	STANDARD;	PRT;	165 AA.
ID	CGHB_HUMAN	STANDARD;		
AC	P01233; Q14000; Q13991;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Choriogonadotropin beta chain precursor (Chorionic gonadotropin beta subunit) (CG-beta).			
GN	CGB.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81012134; PubMed=6774259;			
RA	Fiddes J.C., Goodman H.M.;			
RT	"The cDNA for the beta-subunit of human chorionic gonadotropin suggests evolution of a gene by readthrough into the 3'-untranslated region."			
RL	Nature 286:684-687(1980).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84093590; PubMed=6690982;			
RA	Talmadge K., Vamvakopoulos N.C., Fiddes J.C.;			
RT	"Evolution of the genes for the beta subunits of human chorionic gonadotropin and luteinizing hormone."			
RL	Nature 307:37-40(1984).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84008141; PubMed=6194155;			
RA	Policaastro P., Ovitt C.E., Hoshina M., Fukuoka H., Boothby M.R.,			
RA	Boime I.;			
RT	"The beta subunit of human chorionic gonadotropin is encoded by multiple genes."			

J. Biol. Chem. 258:11492-11499(1983).
[4]
SEQUENCE OF 1-20.
MEDLINE=81117268; PubMed=7462224;
RA Birken S., Fetherston J., Canfield R.E., Boime I.;
RT "The amino acid sequences of the prepeptides contained in the alpha
RL and beta subunits of human chorionic gonadotropin.";
[5]
J. Biol. Chem. 256:1816-1823(1981).
[6]
SEQUENCE OF 21-165.
MEDLINE=75211304; PubMed=1150658;
RA Morgan F.J., Birken S., Canfield R.E.;
RT "The amino acid sequence of human chorionic gonadotropin. The alpha
RL subunit and beta subunit.";
[7]
J. Biol. Chem. 250:5247-5258(1975).
[8]
PRELIMINARY SEQUENCE OF 21-165.
MEDLINE=74011267; PubMed=4793659;
RA Carlsen R.B., Bahl O.P., Swaminathan N.;
RT "Human chorionic gonadotropin. Linear amino acid sequence of the beta
RL subunit.";
[9]
J. Biol. Chem. 248:6810-6827(1973).
[10]
SEQUENCE OF 1-5 FROM N.A.
MEDLINE=86195987; PubMed=2422163;
RA Policastro P.F., Daniels-McQueen S., Carle G., Boime I.;
RT "A map of the hCG beta-LH beta gene cluster.";
[11]
J. Biol. Chem. 261:5907-5916(1986).
[12]
PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
MEDLINE=81215630; PubMed=7240231;
RA Mise T., Bahl O.P.;
RT "Assignment of disulfide bonds in the beta subunit of human chorionic
RL gonadotropin.";
[13]
J. Biol. Chem. 256:6587-6592(1981).
[14]
DISULFIDE BONDS.
MEDLINE=90094415; PubMed=1688430;
RA Saccuzo Beebe J., Mountjoy K., Krzesicki R.F., Perini F.,
RA Raddon R.W.;
RT "Role of disulfide bond formation in the folding of human chorionic
RL gonadotropin beta subunit into an alpha beta dimer assembly-competent
form.";
[15]
J. Biol. Chem. 265:312-317(1990).
[16]
STRUCTURE OF CARBOHYDRATES.
MEDLINE=92314469; PubMed=1820200;
RA Weisshaar G., Hiyama J., Renwick A.G.C.;
RT "Site-specific N-glycosylation of human chorionic gonadotropin --
RL structural analysis of glycopeptides by one- and two-dimensional 1H
NMR spectroscopy.";
[17]
Glycobiology 1:393-404(1991).
[18]
X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
MEDLINE=94261179; PubMed=8202136;
RA Laphorn A.J., Harris D.C., Littlejohn A., Lustbader J.W.,
RA Canfield R.E., Machin K.J., Morgan F.J., Isaacs N.W.;
RT "Crystal structure of human chorionic gonadotropin.";
RL Nature 369:455-461(1994).
CC -!- FUNCTION: STIMULATES THE OVARIAN TO SYNTHESIZE THE STEROIDS THAT
CC ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- TISSUE SPECIFICITY: PLACENTA.
CC -!- DEVELOPMENTAL STAGE: MADE BY THE FIRST TRIMESTER PLACENTA.
CC -!- PHARMACEUTICAL: Available under the names Novarel (Ferring) and
CC Profasi (Serono).
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.

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DR EMBL; J00117; AAA96690.1; -;
DR EMBL; X00265; CAA25068.1; ALT_INIT.
DR EMBL; X00266; CAA25069.1; ALT_INIT.
DR EMBL; M13504; AAA52005.1; -;
DR EMBL; M13505; AAA52008.1; -;
DR EMBL; M13503; AAA52009.1; -;
DR EMBL; K03189; AAA53288.1; -;
DR EMBL; K03187; AAA53288.1; JOINED.
DR EMBL; K03188; AAA53288.1; JOINED.
DR EMBL; K03183; AAA53287.1; -;
DR EMBL; K00092; AAA53287.1; JOINED.
DR EMBL; K03182; AAA53287.1; JOINED.
DR PIR; A01502; KTHUB.
DR PDB; 1HCN; 30-SEP-94.
DR PDB; 1HRP; 01-NOV-94.
DR PDB; 1XUL; 15-MAY-97.
DR GlycoSuiteDB; P01233; -;
DR Genew; HGNC:1886; CGB.
DR Genew; HGNC:16451; CGB7.
DR Genew; HGNC:16452; CGB5.
DR MIM; 118860; -;
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR002400; GF_cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Glycoprotein; Signal; Pharmaceutical; 3D-structure.
FT SIGNAL 1 20 CHORIOGONADOTROPIN BETA CHAIN.
FT CHAIN 21 165
FT DISULFID 29 77
FT DISULFID 43 92
FT DISULFID 46 130
FT DISULFID 54 108
FT DISULFID 58 110
FT DISULFID 113 120
FT CARBOHYD 33 33
FT CARBOHYD 50 50
FT CARBOHYD 141 141
FT CARBOHYD 147 147
FT CARBOHYD 152 152
FT CARBOHYD 158 158
FT VARIANT 137 137
FT CONFLICT 24 24
FT SEQUENCE 165 AA; 17739 MW; 5598FB951A05748 CRC64;
Query Match 100.0%; Score 86; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTRVLQGVLPALPQVVC 17
DB 61 MTRVLQGVLPALPQVVC 77

RESULT 2
LSHB_HUMAN
ID LSHB_HUMAN STANDARD; PRT; 141 AA.
AC P01229;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
 DE beta) (LSH-B) (LH-B).
 GN LHB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=84093590; PubMed=6690982;
 RA Talmadge K., Vanvakopoulos N.C., Fiddes J.C.;
 RA "Evolution of the genes for the beta subunits of human chorionic
 RT gonadotropin and luteinizing hormone.";
 RL Nature 307:37-40(1984).
 RN [2]
 RN SEQUENCE OF 21-141.
 RP MEDLINE=76062547; PubMed=1191677;
 RA Saram M.R., Li C.H.;
 RA "Human pituitary lutropin. Isolation, properties, and the complete
 RT amino acid sequence of the beta-subunit.";
 RL Biochim. Biophys. Acta 412:70-81(1975).
 RN [3]
 RN PRELIMINARY SEQUENCE OF 21-141.
 RP MEDLINE=73090987; PubMed=4685398;
 RA Shome B., Parlow A.F.;
 RA "The primary structure of the hormone-specific, beta subunit of human
 RT pituitary luteinizing hormone (hLH).";
 RL J. Clin. Endocrinol. Metab. 36:618-621(1973).
 RN [4]
 RN PRELIMINARY PARTIAL SEQUENCE.
 RP MEDLINE=73221227; PubMed=4719207;
 RA Closset J., Hennen G., Leguin R.M.;
 RA "Human luteinizing hormone. The amino acid sequence of the
 RT subunit.";
 RL FEBS Lett. 29:97-100(1973).
 RN [5]
 RN STRUCTURE OF CARBOHYDRATE.
 RP MEDLINE=91122088; PubMed=1991473;
 RA Weisshaar G., Hiyama J., Renwick A.G.C., Nimtz M.;
 RA "NMR investigations of the N-linked oligosaccharides at individual
 RT glycosylation sites of human lutropin.";
 RL Eur. J. Biochem. 195:257-268(1991).
 RN [6]
 RN STRUCTURE BY NMR OF 58-77.
 RP MEDLINE=92357029; PubMed=1495492;
 RA Keutmann H.T., Hua Q.-X., Weiss M.A.;
 RA "Structure of a receptor-binding fragment from human luteinizing
 RT hormone beta-subunit determined by [1H]- and [15N]nuclear magnetic
 resonance spectroscopy.";
 RL Mol. Endocrinol. 6:904-913(1992).
 RN [7]
 RN VARIANT ARG-74.
 RP MEDLINE=92085985; PubMed=1727547;
 RA Weiss J., Axelrod L., Whitcomb R.W., Harris P.E., Crowley W.F.,
 RA Jameson J.L.;
 RA "Hypogonadism caused by a single amino acid substitution in the beta
 RT subunit of luteinizing hormone.";
 RL New Engl. J. Med. 326:179-183(1992).
 CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
 CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
 CC CHAIN WHICH CONFERES BIOLOGICAL SPECIFICITY TO THYROTROPIN,
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -!- TISSUE SPECIFICITY: PITUITARY.
 CC -!- DISEASE: DEFECTS IN LHB ARE A CAUSE OF HYPOGONADISM WHICH IS
 CC CHARACTERIZED BY INFERTILITY AND PSEUDOPHERMAPRODITISM.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
 CC FAMILY.
 CC
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 or send an email to license@isb-sib.ch).

 CC EMBL; X00264; CA225067.1; -
 CC EMBL; S71273; AADI4960.1; ALT_SEQ.
 CC PIR; A01497; UTHUB.
 CC HSSP; P01233; 1XUL.
 CC GlycoSuiteDB; P01229; -
 CC Genew; HGNC:6584; LHB.
 CC MIM; 152780; -
 CC InterPro; IPR000359; Cys_knot.
 CC InterPro; IPR002400; GF_cys_knot.
 CC InterPro; IPR001545; Gly_hormoneB.
 CC Pfam; PF00007; Cys_knot; 1.
 CC PRINTS; PR00438; GFCYSKNOT.
 CC SMART; SM00068; GHb; 1.
 CC PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 CC PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 CC Hormone; Glycoprotein; Signal; Pseudohermaphroditism;
 CC Disease mutation.
 FT SIGNAL 1 20
 FT CHAIN 21 141 LUTROPIN BETA CHAIN.
 FT DISULFID 29 77 BY SIMILARITY.
 FT DISULFID 43 92 BY SIMILARITY.
 FT DISULFID 46 130 BY SIMILARITY.
 FT DISULFID 54 108 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 113 120 BY SIMILARITY.
 FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .).
 FT VARIANT 74 74 /FTIQ-CAR_000045.
 FT /Q -> R (IN HYPOGONADISM; LACK OF
 FT RECEPTOR-BINDING).
 FT /FTIQ-VAR_003189.
 FT CONFLICT 39 39 E -> Q (IN REF. 2).
 FT CONFLICT 76 76 MISSING (IN REF. 2).
 FT CONFLICT 132 135 HPQL -> PQH (IN REF. 2).
 SQ SEQUENCE 141 AA; 15345 MW; E4117662531137C CRC64;
 Query Match 80.2%; Score 69; DB 1; Length 141;
 Best Local Similarity 82.4%; Pred. No. 8.e-05;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MTRVLQGVLPALPQVVC 17
 Db 61 MMRVLQAVLPPLPQVVC 77
 RESULT 3
 CGHB_PAPAN
 ID CGHB_PAPAN STANDARD; PRT; 165 AA.
 AC P07434;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Choriogonadotropin beta chain precursor (Chorionic gonadotropin beta
 DE subunit) (CG-beta).
 GN CGB.
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Papio.
 OX NCBI_TaxID=9555;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=87106651; PubMed=2433190;
 RA Crawford R.J., Tregear G.W., Niall H.D.;
 RA "The nucleotide sequences of baboon chorionic gonadotropin
 RT beta-subunit genes have diverged from the human.";
 RL Gene 46:161-169(1986).
 CC -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
 CC ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA

CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- TISSUE SPECIFICITY: PLACENTA.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST FIVE COPIES OF CG-RELATED GENES
CC AND AT LEAST TWO OF THESE ARE EXPRESSED IN THE BABOON PLACENTA.
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL; M14966; AAA35383.1; -
CC PIR; A25808; KTBAB.

CC HSSP; P01233; 1XUL.

CC InterPro; IPR000359; Cys_knot.

CC InterPro; IPR002400; GF_cysknot.

CC Pfam; PF0001545; Gly_hormoneB.

CC PRINTS; PR00438; GFCYSKNOT.

CC SMART; SM00068; GHb; 1.

CC PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.

CC PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.

CC Hormone; Glycoprotein; Signal.

CC SIGNAL 1 20
CC CHAIN 21 165 CHORIOGONADOTROPIN BETA CHAIN.

CC DISULFID 29 77 BY SIMILARITY.

CC DISULFID 43 92 BY SIMILARITY.

CC DISULFID 46 130 BY SIMILARITY.

CC DISULFID 54 108 BY SIMILARITY.

CC DISULFID 58 110 BY SIMILARITY.

CC DISULFID 113 120 BY SIMILARITY.

CC CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (BY SIMILARITY).

CC CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (BY SIMILARITY).

CC CARBOHYD 141 141 O-LINKED (GLCNAC. . .) (BY SIMILARITY).

CC CARBOHYD 147 147 O-LINKED (BY SIMILARITY).

CC CARBOHYD 152 152 O-LINKED (BY SIMILARITY).

CC SEQUENCE 165 AA; 17592 MW; 36D3E207A9F1E1C3 CRC64;

Query Match 76.7%; Score 66; DB 1; Length 165;
Best Local Similarity 76.5%; Pred. No. 0.00034;
Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 61 MVRVLQAVLPVPVQVVC 77

RESULT 4
CGHB_CALJA STANDARD; PRT; 164 AA.

AC P51500;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Choriogonadotropin beta chain precursor (Chorionic gonadotropin beta
DE subunit) (CG-beta).

GN CGB.

OS Callithrix jacchus (Common marmoset).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC Callithrix.

OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96115012; PubMed=7492691;
RA Simula A.P., Amato F., Faast R., Lopata A., Berka J., Norman R.J.;
RT "Luteinizing hormone/chorionic gonadotropin bioactivity in the common

RT marmoset (Callithrix jacchus) is due to a chorionic gonadotropin
RT molecule with a structure intermediate between human chorionic
RT gonadotropin and human luteinizing hormone.";
RL Biol. Reprod. 53:380-389(1995).

CC -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.

CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.

CC -!- TISSUE SPECIFICITY: PLACENTA.

CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.

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CC or send an email to license@isb-sib.ch).

CC EMBL; U04447; AAC00029.1; -
CC HSSP; P01233; 1XUL.

CC InterPro; IPR000359; Cys_knot.

CC InterPro; IPR002400; GF_cysknot.

CC Pfam; PF0001545; Gly_hormoneB.

CC PRINTS; PR00438; GFCYSKNOT.

CC SMART; SM00068; GHb; 1.

CC PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.

CC PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.

CC Hormone; Glycoprotein; Signal.

CC SIGNAL 1 20
CC CHAIN 21 164 CHORIOGONADOTROPIN BETA CHAIN.

CC DISULFID 29 77 BY SIMILARITY.

CC DISULFID 43 92 BY SIMILARITY.

CC DISULFID 46 130 BY SIMILARITY.

CC DISULFID 54 108 BY SIMILARITY.

CC DISULFID 58 110 BY SIMILARITY.

CC DISULFID 113 120 BY SIMILARITY.

CC CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (BY SIMILARITY).

CC CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (BY SIMILARITY).

CC CARBOHYD 151 151 O-LINKED (BY SIMILARITY).

CC SEQUENCE 164 AA; 17712 MW; 0CD92EDDC2618FA6 CRC64;

Query Match 70.9%; Score 61; DB 1; Length 164;
Best Local Similarity 70.6%; Pred. No. 0.0024;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 61 MVRVLQAVLPVPVQVVC 77

RESULT 5
LSHB_HORSE STANDARD; PRT; 169 AA.

ID LSHB_HORSE P01234;

AC P08751; P01234;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Lutropin/choriogonadotropin beta chain precursor (LSH-B/CG-B)
DE {luteinizing hormone beta subunit}.

GN LHB.

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92357035; PubMed=1379674;
RA Sherman G.B., Wolfe M.W., Farmerie T.A., Clay C.M.,
RA Threadgill D.S., Sharp D.C., Nilsson J.H.;


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CC
DR EMBL; U25145; AAA92841.1; -.
DR EMBL; Y10418; CAA71445.1; -.
DR HSP; P01233; 1XUL.
DR MGD; MGI:96782; Libb.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHE; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
DR Hormone; Signal; Glycoprotein.
DR SIGNAL; 1
ET 20
BY SIMILARITY.

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 EMBL; D00579; BAA00457.1; -.
 DR PIR; A30322; UTPCB.
 DR PIR; A48170; A48170.

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DR HSSP; P01233; 1XUL.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; P000438; GFCYSKNOT.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Signal; Glycoprotein.
FT SIGNAL 1 20
FT CHAIN 21 141 LUTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC... ).
FT MOD_RES 21 21 BLOCKED.
FT VARIANT 30 30 R -> Z.
FT CONFLICT 40 40 N -> D (IN REF. 3).
FT CONFLICT 62 62 V -> R (IN REF. 3).
FT CONFLICT 83 83 S -> I (IN REF. 3).
FT CONFLICT 87 87 I -> S (IN REF. 3).
FT CONFLICT 122 123 GP -> PG (IN REF. 3).
SQ SEQUENCE 141 AA; 14889 MW; 803BE7C59F3C2CF CRC64;

Query Match 59.3%; Score 51; DB 1; Length 141;
Best Local Similarity 58.8%; Pred. No. 0.11;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MTRVLOGVLPALPQVVC 17
   | | | | | : | | | |
DB 61 MVRVLPALPPVPQVVC 77

RESULT 11
LSHB_RAT
ID LSHB_RAT STANDARD; PRT; 141 AA.
AC P01230;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin beta chain precursor (luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B).
DE LHB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley;
RX MEDLINE=83273673; PubMed=6192440;
RA Chin W.W., Godine J.E., Klein D.R., Chang A.S., Tan L.K.,
RA Habener J.F.;
RT "Nucleotide sequence of the cDNA encoding the precursor of the beta
RT subunit of rat lutropin.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4649-4653(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85080043; PubMed=6096374;
RA Jameson L., Chin W.W., Hollenberg A.N., Chang A.S., Habener J.F.;
RA "The gene encoding the beta-subunit of rat luteinizing hormone.";
RT Analysis of gene structure and evolution of nucleotide sequence.";
RL J. Biol. Chem. 259:15474-15480(1984).
RN [3]
RP SEQUENCE OF 4-141 FROM N.A.
RC STRAIN-Wistar Imamichi; TISSUE=Anterior pituitary;
RA Kato Y., Ezashi T., Hirai T., Kato T.;
RT "Strain difference in nucleotide sequences of rat glycoprotein hormone
RT subunit cDNAs and gene fragment.";

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RL Zool. Sci. 7:877-885(1990).
CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN.
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; V01542; CAA24783.1; -
CC EMBL; J00749; AAA96703.1; -
CC EMBL; D00576; BAA00454.1; -
CC PIR; A01498; UTRTB.
CC PIR; S42527; S42527.
CC HSSP; P01233; 1XUL.
CC InterPro; IPR000359; Cys_knot.
CC InterPro; IPR002400; GF_cysknot.
CC InterPro; IPR001545; Gly_hormoneB.
CC Pfam; PF00007; Cys_knot; 1.
CC PRINTS; P000438; GFCYSKNOT.
CC SMART; SM00068; GHb; 1.
CC PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
CC PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Signal; Glycoprotein.
FT SIGNAL 1 20
FT CHAIN 21 141 LUTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC... ) (PROBABLE).
SQ SEQUENCE 141 AA; 15177 MW; 50796FB8E32F83BF CRC64;

Query Match 59.3%; Score 51; DB 1; Length 141;
Best Local Similarity 58.8%; Pred. No. 0.11;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MTRVLOGVLPALPQVVC 17
   | | | | | : | | | |
DB 61 MVRVLPALPPVPQVVC 77

RESULT 12
LSHB_BOVIN
ID LSHB_BOVIN STANDARD; PRT; 141 AA.
AC P04651;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin beta chain precursor (luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B).
DE LHB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85207729; PubMed=2987241;
RA Virgin J.B., Silver B.J., Thomason A.R., Nilson J.H.;
RT "The gene for the beta subunit of bovine luteinizing hormone encodes
RT a gonadotropin mRNA with an unusually short 5'-untranslated region.";

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RL	J. Biol. Chem. 260:7072-7077(1985).	LSHB_SHEEP	STANDARD;	PRT;	141 AA.
RN	[2]	PO1231;			
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=85182575; PubMed=3838746;				
RX	Maurer R.A.;				
RA	'Analysis of several bovine lutropin beta subunit cDNAs reveals				
RT	RT heterogeneity in nucleotide sequence.';				
RL	J. Biol. Chem. 260:4684-4687(1985).				
RN	[3]				
RP	SEQUENCE OF 21-139.				
RX	MEDLINE=74075724; PubMed=4770795;				
RA	Maguain-Rogister G., Hennen G.;				
RT	'Luteinizing hormone. The primary structures of the beta-subunit from				
RL	bovine and porcine species.';				
RN	Eur. J. Biochem. 39:235-253(1973).				
RP	-I- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING				
RX	THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.				
RA	-I- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA				
RT	CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,				
RL	LUTROPIN, FOLLITROPIN AND GONADOTROPIN.				
RN	-I- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN				
RP	FAMILY.				
RC	-----				
RA	This SWISS-PROT entry is copyright. It is produced through a collaboration				
RT	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
RL	the European Bioinformatics Institute. There are no restrictions on its				
RN	use by non-profit institutions as long as its content is in no way				
RP	modified and this statement is not removed. Usage by and for commercial				
RX	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
RA	or send an email to license@lsb-sib.ch).				
RT	-----				
RL	EMBL; M10077; AAA30623.1; -;				
RN	EMBL; M11506; AAB59267.1; -;				
RP	PIR; A01499; UTBOB.				
RX	HSP; P01233; IXUL.				
RA	GlycoSuiteDB; P04651; -;				
RT	InterPro; IPR000359; Cys_knot.				
RL	InterPro; IPR002400; GF_cysknot.				
RN	InterPro; IPR001545; Gly_hormoneB.				
RP	Pfam; PF00007; Cys_knot; 1.				
RX	PRINTS; PR00438; GFCYSKNOT.				
RA	SMART; SM00068; GHB; 1.				
RT	PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.				
RL	PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.				
RN	Hormone; Signal; Glycoprotein.				
RP	SIGNAL				
RX	CHAIN				
RA	LUTROPIN BETA CHAIN.				
RT	BY SIMILARITY.				
RL	BY SIMILARITY.				
RN	BY SIMILARITY.				
RP	BY SIMILARITY.				
RX	BY SIMILARITY.				
RA	N-LINKED (GLCNAC. . .).				
RT	MISSING (IN REF. 2).				
RL	Q -> E (IN REF. 3).				
RN	P -> S (IN REF. 2).				
RP	GP -> PG (IN REF. 3).				
RX	Q -> E (IN REF. 3).				
RA	SEQUENCE 141 AA; 15202 MW; 44FBACBD4901BC95 CRC64;				
RT	Query Match				
RL	Best Local Similarity				
RN	Matches 10; Conservative 2; Mismatches				
RP	58.1%; Score 50; DB 1; Length 141;				
RX	58.8%; Pred. No. 0.16;				
RA	Indels 0; Gaps 0;				
RT	-----				
RL	QY 1 MTRVLQGVLPALPQVVC 17				
RN	: :				
RP	Db 61 MKRVLPVILPPMPQVVC 77				
RX	-----				
RA	RESULT 13				
RT	LSHB_SHEEP				

DR	EMBL; S64695; AAB27819.1; -.
DR	EMBL; X52486; CAA36729.1; -.
DR	PIR; A01500; UTSBH.
DR	PIR; S09232; S09232.
DR	HSP; P01233; 1XUL.
DR	GlycoSuiteDB; P01231; -.
DR	InterPro; IPR000359; Cys_knot.
DR	InterPro; IPR002400; GF_cysknot.
DR	InterPro; IPR001545; Gly_hormoneB.
DR	Pfam; PF00007; Cys_knot; 1.
DR	PRINTS; PR00438; GFCYSKNOT.
DR	SMART; SM00068; GHb; 1.
DR	PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR	PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW	Hormone; Signal; Glycoprotein.
FT	SIGNAL 1 20
FT	CHAIN 21 141
FT	DISULFID 29 77
FT	DISULFID 43 92
FT	DISULFID 46 130
FT	DISULFID 54 108
FT	DISULFID 58 110
FT	DISULFID 113 120
FT	MOD_RES 21 21
FT	CARBOHYD 33 33
FT	LUTROPIN BETA CHAIN. BY SIMILARITY.
FT	BY SIMILARITY.
FT	BY SIMILARITY.
FT	BLOCKED.
FT	N-LINKED (GLCNAC...).
FT	/FTID-CAR_000046.
FT	MISSING (IN SOME MOLECULES).
FT	Q -> E (IN REF. 4).
FT	L -> P (IN REF. 1).
FT	R -> Q (IN REF. 2).
FT	P -> PP (IN REF. 4).
FT	E -> Q (IN REF. 4).
FT	GP -> PG (IN REF. 3 AND 4).
FT	Q -> E (IN REF. 3 AND 4).
FT	SEQUENCE 141 AA; 15184 MW; C59EC7C0AA55A9DC CRC64;
SQ	
Query Match 58.1%; Score 50; DB 1; Length 141;	
Best Local Similarity 58.8%; Pred.No.0.16;	
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;	

RESULT 14	
LSHB_FELCA	
ID LSHB_FELCA	STANDARD; PRT: 143 AA.
AC Q77805;	
DT 16-OCT-2001	(Rel. 40, Created)
DT 16-OCT-2001	(Rel. 40, Last sequence update)
DT 16-OCT-2001	(Rel. 40, Last annotation update)
DE Lutropin beta chain precursor	(Lutealizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B).	
GN LHB.	
OS Felis silvestris catus (Cat).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.	
OX NCBI_TaxId=9685;	
[1]	
RN SEQUENCE FROM N.A.	
RP TISSUE=pituitary;	
RA pukazhenhi B.S., Varma G.M., Brown J.L.;	
RC "Molecular cloning and sequence analysis of the cDNA for the feline	
RT luteinizing hormone beta subunit.";	
RRL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.	
CC -! FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING	
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.	
CC -! SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA	
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,	
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.	
CC -! SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN	
CC FAMILY.	

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CC CC use by non-profit institutions as long as its content is in no way
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CC CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
-----
DR DR EMBL; AF095716; AAC64196.1; -.
DR DR HSSP; P01233; 1XU.
DR DR InterPro; IPR000359; Cys_knot.
DR DR InterPro; IPR002400; GF_cysknot.
DR DR InterPro; IPR001545; Gly_hormoneB.
DR DR Pfam; PF00007; Cys_knot; 1.
DR DR PRINTS; PR00438; GFCYSKNOT.
DR DR SMART; SM00068; GHB; 1.
DR DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
DR DR Hormone; Signal; Glycoprotein.
FT FT SIGNAL 1 22 BY SIMILARITY.
FT FT CHAIN 23 143 LUTROPIN BETA CHAIN.
FT FT DISULFID 31 79 BY SIMILARITY.
FT FT DISULFID 45 94 BY SIMILARITY.
FT FT DISULFID 48 132 BY SIMILARITY.
FT FT DISULFID 56 110 BY SIMILARITY.
FT FT DISULFID 60 112 BY SIMILARITY.
FT FT DISULFID 115 122 BY SIMILARITY.
FT FT CARBOHYD 35 35 N-LINKED (GLCNAC..)(POTENTIAL).
SQ SEQUENCE 143 AA; 15318 MW; C5C55DDC907422DB CRC64;

Query Match 58.1%; Score 50; DB 1; Length 143;
Best Local Similarity 58.8%; Pred. No. 0.16;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MTRVLQGVLPALPQVC 17
    I I I I I I I I I I I I
Db 63 MMRVLPALPPVQPVC 79

RESULT 15
LSHB_EQUAS
ID LSHB_EQUAS STANDARD; PRT; 169 AA.
AC P19794;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Lutropin/choriogonadotropin beta chain precursor (LSH-B/CG-B)
DE (Lutenizing hormone beta subunit).
GN LHB.
OS Equus asinus (Donkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9793;
RN [1]
RP SEQUENCE FROM N.A.
RA Chopineau M., Combarnous Y., Allen W.R., Stewart F.;
RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP PRELIMINARY SEQUENCE OF 105-169 FROM N.A.
RC TISSUE=placenta;
RX MEDLINE=90262634; PubMed=2344391;
RT Leigh S.E.A., Stewart F.;
RT "Partial cDNA sequence for the donkey chorionic gonadotrophin-beta
RT subunit suggests evolution from an ancestral LH-beta gene.";
RT J. Mol. Endocrinol. 4:143-150(1990)
CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC CC FAMILY.

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EMBL; X80116; CAA56422.1; ~
EMBL; X53669; CAA37709.1; ALT_SEQ.
PIR; S15676;
HSP; P01233; 1XUL.
InterPro; IPR000359; Cys_knot.
InterPro; IPR002400; GF_cysknot.
InterPro; IPR001545; Gly_hormoneB.
Pfam; PF00007; Cys_knot; 1.
PRINTS; PR00438; GFCYSKNOT.
SMART; SM00068; GHb; 1.
PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
Hormone; Glycoprotein; Signal.
Signal 1 20 BY SIMILARITY.
CHAIN 21 169 LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
DISULFID 29 77 BY SIMILARITY.
DISULFID 43 92 BY SIMILARITY.
DISULFID 46 130 BY SIMILARITY.
DISULFID 54 108 BY SIMILARITY.
DISULFID 58 110 BY SIMILARITY.
DISULFID 113 120 BY SIMILARITY.
CARBOHYD 33 33 N-LINKED (GLCNAC... ) (PROBABLE).
SEQUENCE 169 AA; 17943 MW; AEEP20891E96FA7C CRG64;

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FT 33 N-LINKED (GLCNAC... ) (PROBABLE) .
SQ SEQUENCE 169 AA; 17943 MW; AEED20891E96FA7C CRC64;

Query Match 58.1%; Score 50; DB 1; Length 169;
Best Local Similarity 52.9%; Pred. NO. 0.19;
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

1 MTRVLQGVLPALPOVVC 17
      |||: ||| |||
61 WYEVWPAALPRTPOVVC 77

```

DB	61	MVRNMPAALPPIQPVC	77
RESULT	16		
LSHB_EQUUB			
ID	LSHB_EQUUB	STANDARD;	PRT; 169 AA.
AC	Q46641;		
DT	15-DEC-1998	(Rel. 37, Created)	
DT	15-DEC-1998	(Rel. 37, Last sequence update)	
DT	15-JUN-2002	(Rel. 41, Last annotation update)	
DE	Lutropin/choriogonadotropin beta chain precursor	(LSH-B/CG-B)	
DE	(Luteinizing hormone beta subunit).		
GN	LBH.		
OS	Equus burchelli (Plains zebra) (Equus quagga).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.		
OX	NCBI_TaxID=9790;		
[1]			
RN	SEQUENCE FROM N.A.		
RP	TISSUE=Pituitary;		
RC	MEDLINE=99273280; Pubmed=10341734;		
RX	Chopinseau M., Martinat N., Pourchet C., Stewart F., Combarnous Y.,		
RA	Guillou F.;		
RA	"Cloning, sequencing and functional expression of zebra (Equus		
RT	burchelli) LH".		
RT	J. Reprod. Fert. 115:159-166(1999).		
RL	-1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING		
CC	THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.		
CC	-1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA		
CC	CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,		
CC	LUTROPIN, FOLLITROPIN AND GONADOTROPIN.		
CC	-1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN		
CC	FAMILY.		

FT	DISULFID	34	88	BY SIMILARITY.				
FT	DISULFID	38	90	BY SIMILARITY.				
FT	DISULFID	93	100	BY SIMILARITY.				
FT	CARBOHYD	13		N-LINKED (GLCNAC...).				
SQ	SEQUENCE	118 AA;	12412 MW;	81177A56382F15E7 CRC64;				
Query Match. 57.08; Score 49; DB 1; Length 118;								
Best Local Similarity 52.98; Pred. No. 0.2;								
Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;								
QY	1	MTRVLQGVLPALPQVVC	17					
DB	41	MVRVLPAAALPFVPZPVC	57					
RESULT 19								
LSHB_CRSI STANDARD; PRT; 141 AA.								
ID	LSHB_CRSI	STANDARD;	PRT;	141 AA.				
AC	O77835;	Q19102;						
DT	16-OCT-2001	(Rel. 40, Created)						
DT	16-OCT-2001	(Rel. 40, Last sequence update)						
DT	16-OCT-2001	(Rel. 40, Last annotation update)						
DE	Lutropin beta chain precursor (luteinizing hormone beta subunit) (LSH-beta) (LSH-B).							
DE	beta) (LSH-B) (LH-B).							
GN	LHBI and LHBI.							
OS	Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.							
NCBI_TaxID	=9807;							
RRN	[1]							
RRN	SEQUENCE FROM N.A.							
RRN	MEDLINE=98389253; PubMed=9723860;							
RRN	Lund L.A.; Sherman G.B.;							
RRN	"Duplication of the southern white rhinoceros (Ceratotherium simum							
RRN	simum) luteinizing hormone beta subunit gene.";							
RRN	J. Mol. Endocrinol. 21:19-30(1998).							
RRN	[2]							
RRN	SEQUENCE OF 7-141 FROM N.A.							
RRN	TISSUE=Pituitary;							
RRN	MEDLINE=97449288; PubMed=9305757;							
RRN	Sherman G.B.; Lund L.A.; Bunick D.; Winn R.J.;							
RRN	"Characterization and phylogenetic significance of rhinoceros							
RRN	luteinizing hormone beta (LHbeta) subunit messenger RNA structure,							
RRN	complementary DNA sequence and gene copy number.";							
RRN	Gene 195:131-139(1997).							
CC	-1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING							
CC	THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.							
CC	-1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA							
CC	CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,							
CC	LUTROPIN, FOLLITROPIN AND GONADOTROPIN.							
CC	-1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN							
CC	FAMILY.							

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or send an email to license@isb-sib.ch).								

RR	EMBL;	AF024521;	AAC36049.1;	-				
RR	EMBL;	AF024520;	AAC36048.1;	-				
RR	EMBL;	U72659;	ABE71963.1;	-				
RR	HSSP;	P01233;	1XUL.					
RR	InterPro;	IPR000359;	Cys_knot.					
RR	InterPro;	IPR002400;	GF_cysknot.					
RR	Pfam;	PF0001545;	Gly_hormoneb.					
RR	Pfam;	PF000007;	Cys_knot.1					
RR	PRINTS;	PR00438;	GFCYSKNOT.					
RR	SMART;	SM00068;	GHB;	1.				
RR	PROSITE;	PS00261;	GLYCO_HORMONE_BETA_1;	1.				
RR	PROSITE;	PS00689;	GLYCO_HORMONE_BETA_2;	1.				

Hormone; Signal; Glycoprotein.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 141 LUTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 22 22 R -> K (IN REF. 2).
SQ SEQUENCE 141 AA; 14930 MW; PFEDB157C51976C9 CRC64;

Query Match 57.0%; Score 49; DB 1; Length 141;
Best Local Similarity 58.8%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
| | | | |
Db 61 MVRVLPALPPAPQVVC 77

RESULT 20
LSHB_TRIVU
ID LSHB_TRIVU STANDARD; PRT; 141 AA.
AC 046482;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-beta) (LSH-B) (LH-B).
GN LHB.
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Plutary;
RX MEDLINE=98345424; PubMed=9680394;
RA Harrison G.A., Deane E.M., Cooper D.W.;
RT "cDNA cloning of luteinizing hormone subunits from brushtail possum and red kangaroo."
RL Mamm. Genome 9:638-642(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lawrence S.B., McNatty K.P., Fidler A.E.;
RA Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN FAMILY.
CC
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CC
CC EMBL; AF017448; AAC96019.1; -
CC EMBL; AF090388; AAC63326.1; -
CC HSSP; P01233; 1XUL.
CC InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.

Hormone; Signal; Glycoprotein.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 141 LUTROPIN BETA CHAIN.
FT DISULFID 30 78 BY SIMILARITY.
FT DISULFID 44 93 BY SIMILARITY.
FT DISULFID 47 131 BY SIMILARITY.
FT DISULFID 55 109 BY SIMILARITY.
FT DISULFID 59 111 BY SIMILARITY.
FT DISULFID 114 121 BY SIMILARITY.
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 141 AA; 15060 MW; C6CF98036B3C4EE0 CRC64;

Query Match 57.0%; Score 49; DB 1; Length 141;
Best Local Similarity 58.8%; Pred. No. 0.23;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
| | | | |
Db 62 MVRVLPALPPQVVC 78

RESULT 21
UL16_EBV
ID UL16_EBV STANDARD; PRT; 336 AA.
AC P03221;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE BGLF2 protein.
DE BGLF2.
GN Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
OS Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J., Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C., Tuffnell P.S., Barrell B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome."
RL Nature 310:207-211(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92113548; PubMed=1662696;
RA Chen M.R., Hsu T.Y., Lin S.W., Chen J.Y., Yang C.S.;
RT "Cloning and characterization of cDNA clones corresponding to transcripts from the BamHI G region of the Epstein-Barr virus genome and expression of BGLF2".
RL J. Gen. Virol. 72:3047-3055(1991).
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL16, HSV-6 ORF11R, EBV-1 46, HCMV UL94, EBV BDLF2, AND VZV 44.
CC
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CC
CC EMBL; M60514; AAA45871.1; -
CC EMBL; V01555; CAA24831.1; -
CC EMBL; S77132; AAB21113.1; -
CC PIR; A03784; Q0BE40.
DR PIR; S33036; S33036.
DR InterPro; IPR004286; UL16_UL94.
DR Pfam; PF03044; UL16_UL94; 1.
DR Late protein.
KW SEQUENCE 336 AA; 36888 MW; 840537A416D5584C CRC64;

Query Match 50.0%; Score 43; DB 1; Length 336;
Best Local Similarity 58.8%; Pred. No. 6;

Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MTRVQGVLPALPQVVC 17
I:||||| :|
Db 287 MSRVQGVLPALPQVVC 303

RESULT 22
Z294_HUMAN
ID Z294_HUMAN STANDARD; PRT; 1818 AA.
AC O94822;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Zinc finger protein 294.
GN ZNF294 OR KIAA0714.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Kotaki Y., Choi D.-K., Soeda E.,
RA Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
RA Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordstiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloeker H.,
RA Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
RA Wehmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Leinhardt H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
RN [2]
RP SEQUENCE OF 707-1818.
RX TISSUE=Brain;
RA MEDLINE=99087487; PubMed=9872452;
RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
RA Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XI.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res 5:277-286(1998).
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
CC -!- SIMILARITY: STRONG, TO YEAST YMR247C.
CC
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CC
CC EMBL; AL163249; CAB90430.1; -
CC DR EMBL; AL163248; CAB90429.3; -
CC DR EMBL; AB018257; BAA34434.1; -
CC DR Genew; HGNC:13082; ZNF294.
CC DR InterPro; IPR001841; Znf_ring.
CC DR SMART; SM00184; RING; 1.
CC DR PROSITE; PS00518; 2F_RING.1; FALSE_NEG.
CC DR PROSITE; PS00089; 2F_RING_2; 1.
CC Zinc-finger.
FT ZN_RING 1767 1814 RING-TYPE.
SQ SEQUENCE 1818 AA; 205732 MW; 416E3E7D4DACA705 CRC64;

Query Match 50.0%; Score 43; DB 1; Length 1818;
Best Local Similarity 43.8%; Pred. No. 33;
Matches 7; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 2 TRVQGVLPALPQVVC 17
I:||||| :|
Db 142 TETVKGVLPPYPRFC 157

RESULT 23
CYAA_USTMA
ID CYAA_USTMA STANDARD; PRT; 2493 AA.
AC P49606;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Adenylate cyclase (EC 4.6.1.1) (ATP pyrophosphate-lyase) (Adenylyl
DE cyclase).
GN UAC1 OR REM1.
OS Ustilago maydis (Smut fungus).
OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
OX NCBI_TaxID=5270;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=518;
RA MEDLINE=95087882; PubMed=7995519;
RA Gold S., Duncan G., Barrett K., Kronstad J.W.;
RT "CAMP regulates morphogenesis in the fungal pathogen Ustilago
RT maydis.";
RL Genes Dev. 8:2805-2816(1994).
CC -!- FUNCTION: PLAYS ESSENTIAL ROLES IN REGULATION OF CELLULAR
CC METABOLISM BY CAVALYSING THE SYNTHESIS OF A SECOND MESSENGER,
CC CAMP.
CC -!- CATALYTIC ACTIVITY: ATP = 3',5'-cyclic AMP + diphosphate.
CC -!- SIMILARITY: BELONGS TO ADENYL CYCLASE CLASS-3 FAMILY.
CC -!- SIMILARITY: CONTAINS 21 LEUCINE-RICH REPEATS (LRR).
CC -!- SIMILARITY: CONTAINS 1 PP2C-LIKE DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L33918; AAA57469.1; -
CC DR InterPro; IPR001054; G_cyclase.
CC DR InterPro; IPR001611; LRR.
CC DR InterPro; IPR003592; LRR_out.
CC DR InterPro; IPR003591; LRR_typ.
CC DR InterPro; IPR001932; PP2C-like.
CC DR Pfam; PF00211; guanylate_cyc; 1.
CC DR Pfam; PF00481; PP2C; 1.
CC DR Pfam; PF00560; LRR; 17.
CC DR SMART; SM00044; CYCC; 1.
CC DR SMART; SM00370; LRR; 6.
CC DR SMART; SM00369; LRR_TYP; 2.
CC DR SMART; SM00332; PP2Cc; 1.
CC DR SMART; SM00314; RA; 1.
CC DR PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
CC Lyase; Repeat; Leucine-rich repeat; CAMP synthesis; Magnesium.
FT DOMAIN 759 763 POLY-ASP.
FT REPEAT 1084 1106 LRR 1.
FT REPEAT 1108 1131 LRR 2.
FT REPEAT 1132 1155 LRR 3.
FT REPEAT 1157 1178 LRR 4.
FT REPEAT 1179 1201 LRR 5.
FT REPEAT 1202 1225 LRR 6.
FT REPEAT 1227 1248 LRR 7.
FT REPEAT 1249 1271 LRR 8.
FT REPEAT 1273 1295 LRR 9.
FT REPEAT 1314 1337 LRR 10.

SQ SEQUENCE 2564 AA; 288982 MW; 52CDE7D1D601ECC CRC64;

Query Match 50.0%; Score 43; DB 1; Length 2564;
 Best Local Similarity 61.5%; Pred. No. 46;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 LQGVLPALPQVVC 17
 ||| | |||:|
 Db 604 LQGYPCDPQVIC 616

RESULT 25
 TFR2_HUMAN STANDARD; PRT; 801 AA.
 AC Q9UP52; O75422; Q9HA99; Q9NX67;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 GN Transferrin receptor protein 2 (TFR2).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RC TISSUE=Erythrocytes, and Myeloid leukemia cells;
 RX MEDLINE=99340005; PubMed=10409623;
 RA Kawabata H., Yang R., Hiram T., Vuong P.T., Kawano S., Gombart A.F.,
 RA Koefler H.P.;
 RT "Molecular cloning of transferrin receptor 2: a new member of the
 RT transferrin receptor-like family.";
 RT J. Biol. Chem. 274:20826-20832(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
 RX MEDLINE=99018118; PubMed=9799793;
 RA Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,
 RA Tsui L.-C., Rosenthal A.;
 RT "Large scale analysis of two regions in human chromosome 7q22:
 RT annotation of 650 kb of genomic sequence around the EPO and CUG1 loci
 RT reveals 17 genes.";
 RT Genome Res. 8:1060-1073(1998).
 RN [3]
 RP SEQUENCE OF 1-158 AND 370-801 FROM N.A.
 RC TISSUE=Carcinoma, and Embryo;
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
 RA Wagatsuma M., Hosoliri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
 RA Ninomiya K., Iwayanagi T.;
 RT "NED0 human cDNA sequencing project.";
 RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP DISEASE.
 RX MEDLINE=20264357; PubMed=10802645;
 RA Camaschella C., Roetto A., Cali A., De Gobbi M., Garozzo G.,
 RA Carella M., Majorano N., Totaro A., Gasparini P.;
 RT "The gene TFR2 is mutated in a new type of haemochromatosis mapping to
 RT 7q22.";
 RT Nat. Genet. 25:14-15(2000).
 RN [5]
 RP VARIANT HFE3 LYS-172.
 RX MEDLINE=21213521; PubMed=11313241;
 RA Roetto A., Totaro A., Piperno A., Piga A., Longo F., Garozzo G.,
 RA Cali A., De Gobbi M., Gasparini P., Camaschella C.;
 RT "New mutations inactivating transferrin 2 in hemochromatosis type
 RT 3.";
 RL Blood 97:2555-2560(2001).
 CC -!- FUNCTION: Mediates cellular uptake of transferrin-bound iron in a
 CC non-iron dependent manner. May be involved in iron metabolism,
 CC hepatocyte function and erythrocyte differentiation.

CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. The beta isoform
 CC lacks the transmembrane domain and is probably intracellular.
 CC -!- ALTERNATIVE PRODUCTS: 3 isoforms; alpha (shown here), beta and
 CC gamma, are produced by alternative splicing.
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in liver. While the
 CC alpha form is also expressed in spleen, lung, muscle, prostate and
 CC peripheral blood mononuclear cells, the beta form is expressed in
 CC all tissues tested, albeit weakly.
 CC -!- DISEASE: Defects in TFR2 are a cause of hereditary hemochromatosis
 CC type III (HFE3). HFE3 is a disorder of iron hemostasis resulting
 CC in iron overload and has a phenotype indistinguishable from that
 CC of hereditary hemochromatosis (HH). HH is characterized by
 CC abnormal intestinal iron absorption and progressive increase of
 CC total body iron, which results in midlife in clinical
 CC complications including cirrhosis, cardiopathy, diabetes,
 CC endocrine dysfunctions, arthropathy, and susceptibility to liver
 CC cancer. Since the disease complications can be effectively
 CC prevented by regular phlebotomies, early diagnosis is most
 CC important to provide a normal life expectancy to the affected
 CC subjects.
 CC -!- MISCELLANEOUS: The variant lys-172 found in hereditary
 CC hemochromatosis type III affects the putative initiation codon of
 CC the beta isoform thus preventing its translation.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M28B.
 CC -----
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 CC -----
 CC EMBL: AF067864; AAC45561.1; -
 CC EMBL: AF053356; AAC78796.1; -
 CC EMBL: AK022002; BAB13951.1; -
 CC EMBL: AK000421; BAA91153.1; ALT_INIT.
 CC HSP: P02786; ICBX.
 CC MEROPS: M28.973; -
 CC Genes: HGNC:11762; TFR2.
 CC MIM: 604720; -
 CC MIM: 604250; -
 CC InterPro: IPR003137; PA.
 CC Pfam: PF02225; PA; 1.
 CC Transmembrane; Glycoprotein; Receptor; Signal-anchor;
 CC Alternative splicing; Disease mutation.
 CC DOMAIN 1 83
 CC TRANSMEM 84 104
 CC SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC (POTENTIAL).
 CC EXTRACELLULAR (POTENTIAL).
 CC ENDOCYTOSIS SIGNAL (POTENTIAL).
 CC INTERCHAIN (POTENTIAL).
 CC INTERCHAIN (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC MISSING (IN ISOFORM BETA).
 CC MISSING (IN ISOFORM GAMMA).
 CC M -> K (IN HFE3).
 CC /FTID=VAR_012738.
 CC R -> RIPLSAQV (IN REF. 2).
 CC D3D3082BA835413A CRC64;

Query Match 48.8%; Score 42; DB 1; Length 801;
 Best Local Similarity 64.3%; Pred. No. 21;
 Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 RVLQGVLPALPQV 16
 :||| |||:
 Db 609 KVLQGRLPAAQV 622

. . .

Wed Dec 4 11:39:35 2002

us-09-821-380-1.rsp

Page 17

Search completed: December 4, 2002, 11:26:32
Job time : 10.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:24:20 ; Search time 30.175 Seconds
(without alignments)
116.083 Million cell updates/sec

Title: us-09-821-380-1

Perfect score: 86
Sequence: 1 MTRVLQGVLPALPQVVC 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database :

SPTREMBL21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	159	4 Q8WXL4	Q8wxl4 homo sapien
2	86	100.0	159	4 Q8WXL3	Q8wxl3 homo sapien
3	86	100.0	159	4 Q8WXL2	Q8wxl2 homo sapien
4	86	100.0	159	4 Q8WXL1	Q8wxl1 homo sapien
5	86	100.0	159	4 Q8WTT5	Q8wtt5 homo sapien
6	75	87.2	136	6 Q8WNB8	Q8wnb8 pongo pygma
7	75	87.2	157	6 Q8WNC7	Q8wnc7 pongo pygma
8	75	87.2	157	6 Q8WNC6	Q8wnc6 pongo pygma
9	75	87.2	157	6 Q8WNC5	Q8wnc5 pongo pygma
10	75	87.2	157	6 Q8WNC4	Q8wnc4 pongo pygma
11	69	80.2	136	4 Q8WXL0	Q8wxl0 homo sapien
12	68	79.1	157	6 Q8WNC2	Q8wnc2 presbytis o
13	68	79.1	157	6 Q8WNB9	Q8wnb9 presbytis o
14	66	76.7	159	6 Q8WNB3	Q8wnb3 colobus que
15	66	76.7	159	6 Q8WNB1	Q8wnb1 colobus que
16	66	76.7	159	6 Q8WNB0	Q8wnb0 macaca mula

17	66	76.7	159	6	Q8WNA9	Q8wna9 macaca mula
18	66	76.7	159	6	Q8BEH1	Q8beh1 macaca fasc
19	65	75.6	136	6	Q8WNB6	Q8wnb6 presbytis o
20	63	73.3	156	6	Q8WNA6	Q8wna6 aotus trivi
21	62	72.1	156	6	Q8WNA7	Q8wna7 callicebus
22	62	72.1	157	6	Q8WNC3	Q8wnc3 presbytis o
23	62	72.1	157	6	Q8WNC1	Q8wnc1 presbytis o
24	62	72.1	159	6	Q8WNB4	Q8wnb4 colobus que
25	62	72.1	159	6	Q8WNB2	Q8wnb2 colobus que
26	62	72.1	159	6	Q8WNA8	Q8wna8 macaca mula
27	58	67.4	136	6	Q8WNB5	Q8wnb5 colobus que
28	57	66.3	165	6	Q9GL37	Q9gl37 macaca mula
29	57	66.3	165	11	Q99P48	Q99p48 mus musculu
30	56	65.1	165	6	Q9BEH2	Q8beh2 macaca fasc
31	55	64.0	136	6	Q8WNB7	Q8wnb7 macaca mula
32	54	62.8	157	6	Q8WNC0	Q8wnc0 presbytis o
33	51	59.3	80	11	O63013	O63013 rattus norv
34	51	59.3	136	6	Q8WNA5	Q8wna5 tarsius ban
35	51	59.3	136	6	Q8WNA4	Q8wna4 daubentonla
36	51	59.3	136	6	Q8WNA2	Q8wna2 galago sene
37	51	59.3	136	6	Q8WNA1	Q8wna1 loris tardi
38	51	59.3	136	6	Q8WNA0	Q8wna0 cynocephalu
39	51	59.3	136	6	Q8WNN9	Q8wnn9 pteropus ly
40	51	59.3	141	6	Q8WNI8	Q8wni8 alluropoda
41	50	58.1	89	6	O46619	O46619 equus hemio
42	50	58.1	136	6	Q8WNA3	Q8wna3 lemur varie
43	50	58.1	139	11	O62778	O62778 rattus norv
44	50	58.1	142	6	Q9BDI9	Q9bdi9 panthera ti
45	49	57.0	141	6	O95J85	O95j85 monodelphis
46	47	54.7	82	6	O46622	O46622 ceratotheri
47	46	53.5	393	10	Q9XHB3	Q9xbh3 chusquea ox
48	45	52.3	89	6	O46618	O46618 equus zebra
49	44	51.2	532	16	P72605	P72605 synecocyst
50	43	50.0	237	4	Q9POE9	Q9poe9 homo sapien
51	43	50.0	304	10	Q9SUC9	Q9suc9 arabidopsis
52	43	50.0	336	12	Q8UZF6	Q8uzf6 cercopithec
53	43	50.0	338	16	Q8U8Q7	Q8u8q7 agrobacteri
54	43	50.0	354	4	Q9H8M4	Q9hm4 homo sapien
55	43	50.0	630	4	Q9NUY5	Q9nuy5 homo sapien
56	43	50.0	2561	11	Q8VIE5	Q8vie5 mus musculu
57	42	49.4	343	5	Q9VSZ4	Q9vsz4 drosophila
58	42	49.4	349	5	Q8SXJ3	Q8sxj3 drosophila
59	42	48.8	444	16	Q98IL7	Q98il7 rhizobium l
60	42	48.8	447	16	Q8ZHW4	Q8zh4 versinia pe
61	41	47.7	102	5	Q9XTC5	Q9xtc5 caenothabdi
62	41	47.7	206	16	Q9I706	Q9i706 pseudomonas
63	41	47.7	234	5	Q8STR2	Q8str2 encephalito
64	41	47.7	353	17	Q9HNV1	Q9hmv1 halobacteri
65	41	47.7	432	16	Q930T8	Q930t8 rhizobium m

ALIGNMENTS

RESULT 1	Q8WXL4	Q8WXL4	PRELIMINARY;	PRT;	159 AA.
ID	Q8WXL4	Q8WXL4			
AC	Q8WXL4	Q8WXL4			
DT	01-MAR-2002 (TREMREL. 20, Created)				
DT	01-MAR-2002 (TREMREL. 20, Last sequence update)				
DT	01-JUN-2002 (TREMREL. 21, Last annotation update)				
DE	Chorionic gonadotropin beta subunit (Fragment).				
GN	CGB.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Maston G.A., Ruvalo M.;				
RT	"Chorionic gonadotropin has a recent origin in primates and an evolutionary history of selection.";				
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.				

```

DR EMBL; AF397576; AAL69704.1; -.
DR InterPro; IPR000359; Cys_knot.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA; 16909 MW; A598A73CC97B57EE CRC64;

Query Match 100.0%; Score 86; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 56 MTRVLQGVLPALPQVVC 72

RESULT 2
Q8WXL3 PRELIMINARY; PRT; 159 AA.
ID Q8WXL3
AC Q8WXL3;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A.; Ruvoilo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397576; AAL69706.1; -.
DR InterPro; IPR000359; Cys_knot.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA; 17006 MW; AFDC4CE2542EC084 CRC64;

Query Match 100.0%; Score 86; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 56 MTRVLQGVLPALPQVVC 72

RESULT 3
Q8WXL2 PRELIMINARY; PRT; 159 AA.
ID Q8WXL2
AC Q8WXL2;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RA Maston G.A.; Ruvoilo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397579; AAL69707.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA; 16960 MW; 24761E38796A1727 CRC64;

Query Match 100.0%; Score 86; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 56 MTRVLQGVLPALPQVVC 72

RESULT 4
Q8WXL1 PRELIMINARY; PRT; 159 AA.
ID Q8WXL1
AC Q8WXL1;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A.; Ruvoilo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397581; AAL69709.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA; 16969 MW; 3C963B3C3D2E57FF CRC64;

Query Match 100.0%; Score 86; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
Db 56 MTRVLQGVLPALPQVVC 72

RESULT 5
Q8WTT5 PRELIMINARY; PRT; 159 AA.
ID Q8WTT5
AC Q8WTT5;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.

```

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397577; AAL69705.1; -;
 DR EMBL; AF397580; AAL69708.1; -;
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHb; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT 159
 SQ SEQUENCE 159 AA; 16944 MW; 246BA938796A1727 CRC64;

Query Match 100.0%; Score 86; DB 4; Length 159;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
 ||||| ||||| |||||
 Db 56 MTRVLQGVLPALPQVVC 72

RESULT 6
 Q8WNB8 PRELIMINARY; PRT; 136 AA.
 AC Q8WNB8;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Luteinizing hormone beta subunit (Fragment).
 GN LHB.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397592; AAL69720.1; -;
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHb; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 136 AA; 14708 MW; 11F17052CF0DEFB9 CRC64;

Query Match 87.2%; Score 75; DB 6; Length 136;
 Best Local Similarity 88.2%; Pred. No. 8.7e-05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
 ||||| ||||| |||||
 Db 56 MTRVLQGVLPALPQVVC 72

RESULT 7
 Q8WNC7 PRELIMINARY; PRT; 157 AA.
 AC Q8WNC7;

DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Chorionic gonadotropin beta subunit (Fragment).
 GN CGB.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397582; AAL69710.1; -;
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHb; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT 157
 SQ SEQUENCE 157 AA; 16928 MW; 825D27A00EFBD4F6 CRC64;

Query Match 87.2%; Score 75; DB 6; Length 157;
 Best Local Similarity 88.2%; Pred. No. 0.0001;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
 ||||| ||||| |||||
 Db 56 MTRVLQGVLPALPQVVC 72

RESULT 8
 Q8WNC6 PRELIMINARY; PRT; 157 AA.
 AC Q8WNC6;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Chorionic gonadotropin beta subunit (Fragment).
 GN CGB.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397583; AAL69711.1; -;
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHb; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT 157
 SQ SEQUENCE 157 AA; 16868 MW; 97BD27A014E1D4EC CRC64;

Query Match 87.2%; Score 75; DB 6; Length 157;
 Best Local Similarity 88.2%; Pred. No. 0.0001;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
 ||||| ||||| |||||
 Db 56 MTRVLQGVLPALPQVVC 72

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RESULT 9
Q8WNC5 PRELIMINARY; PRT; 157 AA.
AC Q8WNC5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397584; AAL69712.1; -.
DR InterPro; IPR000359; Cys_knot.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 17027 MW; 8317774E0F4BD4ED CRC64;

Query Match 87.2%; Score 75; DB 6; Length 157;
Best Local Similarity 88.2%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
| | | | | | | | | | | | | | | | | | | | | |
Db 56 MTRVLQSVLPPLPQVVC 72

RESULT 10
Q8WNC4 PRELIMINARY; PRT; 157 AA.
AC Q8WNC4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (fragment).
GN CGB.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397585; AAL69713.1; -.
DR InterPro; IPR000359; Cys_knot.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 16985 MW; 825D27AC3EFD4F6 CRC64;

Query Match 87.2%; Score 75; DB 6; Length 157;
Best Local Similarity 88.2%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
| | | | | | | | | | | | | | | | | | | | | |
Db 56 MTRVLQSVLPPLPQVVC 72
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QY 1 MTRVLQGVLPALPQVVC 17
| | | | | | | | | | | | | | | | | | | | | |
Db 56 MTRVLQSVLPPLPQVVC 72

RESULT 11
Q8WXL0 PRELIMINARY; PRT; 136 AA.
ID Q8WXL0
AC Q8WXL0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Luteinizing hormone beta subunit (Fragment).
GN LHB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397591; AAL69719.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 136
SQ SEQUENCE 136 AA; 14712 MW; FE5451852A45054E CRC64;

Query Match 80.2%; Score 69; DB 4; Length 136;
Best Local Similarity 82.4%; Pred. No. 0.00086;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
| | | | | | | | | | | | | | | | | | | | | |
Db 56 MTRVLQAVLPPLPQVVC 72

RESULT 12
Q8WNC2 PRELIMINARY; PRT; 157 AA.
ID Q8WNC2
AC Q8WNC2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Presbytis obscura.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Presbytis.
OX NCBI_TaxID=78450;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397587; AAL69715.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 157
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SQ SEQUENCE 157 AA; 16773 MW; 17F1B4E17BE57CB3 CRC64;

Query Match 79.1%; Score 68; DB 6; Length 157;
Best Local Similarity 76.5%; Pred. No. 0.0015;
Matches 13; Conservative 1; Mismatches 3; Indels

QY 1 MTRVLQGVLPALPQVVC 17
| | | | | | | : | | | |
Db 56 MMRVLQGVLPVPPOAVC 72

RESULT 13

Q8WNB9	PRELIMINARY;	PRT;	157 AA.
ID	Q8WNB9		
AC	Q8WNB9;		
DT	01-MAR-2002 (TReMBLrel. 20, Created)		
DT	01-MAR-2002 (TReMBLrel. 20, Last sequence update)		
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)		
DE	Chlorionic gonadotropin beta subunit (Fragment).		
GN	GGB.		
OS	Presbytis obscura.		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;		
OC	Presbytis.		
OX	NCBI_TaxID=78450;		
RN	11		

Query Match 79.1%; Score 68; DB 6; Length 157;
Best Local Similarity 76.5%; Pred. No. 0.0015;
Matches 13; Conservative 1; Mismatches 3; Indels

QY 1 MTRVLQGVLPALPQVC 17
| | | | | | | : | | |
Db 56 MMRVLOGVLPVPPOAVC 72

RESULT 14

Q8WNB3	PRELIMINARY;	PRT;	159 AA.
ID	Q8WNB3		
AC	Q8WNB3;		
DT	01-MAR-2002 (TReMBLrel. 20, Created)		
DT	01-MAR-2002 (TReMBLrel. 20, Last sequence update)		
DT	01-JUN-2002 (TReMBLrel. 21, Last annotation update)		
DE	Chorionic gonadotropin beta subunit (Fragment).		
DE	CGB.		
GN	Colobus guereza (Black-and-white colobus monkey).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;		
OC	Colobus.		
OX	NCBI_TaxID=33548;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Maston G.A., Ruvolo M.;		
RT	"Chorionic gonadotropin has a recent origin in primates and an		
RT	evolutionary history of selection.";		
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF397597; AAL69725.1; -		
DR	InterPro; IPR000359; Cys.knot.		

RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397600; AAL69728.1; -;
 DR InterPro; IPR000359; Cys_knot.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHb; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 159
 SQ SEQUENCE 159 AA; 16853 MW; 7B64051C2F863870 CRC64;

Query Match 76.7%; Score 66; DB 6; Length 159;
 Best Local Similarity 76.5%; Pred. No. 0.0032;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
 Db 56 MMRVLQAVLPVPVQVVC 72
 ||||| ||| :|||||

RESULT 17

Q8WNA9 PRELIMINARY; PRT; 159 AA.

AC Q8WNA9;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Chorionic gonadotropin beta subunit (Fragment).
 GN CGB.
 OS Macaca mulatta (rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397601; AAL69729.1; -;
 DR InterPro; IPR000359; Cys_knot.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHb; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 159
 SQ SEQUENCE 159 AA; 16915 MW; 9231691ED0D82863 CRC64;

Query Match 76.7%; Score 66; DB 6; Length 159;
 Best Local Similarity 76.5%; Pred. No. 0.0032;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
 Db 56 MMRVLQAVLPVPVQVVC 72
 ||||| ||| :|||||

RESULT 18

Q9BEH1 PRELIMINARY; PRT; 165 AA.

AC Q9BEH1;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Chorionic gonadotropin beta subunit 2.

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Maston G.A., Matsumoto K., Lasley B.L., Bedows E.;
 RT "A Comparison of Chorionic Gonadotropin Expression by Human and
 Macaque Trophoblast Cells."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY026360; AAK08644.1; -;
 DR HSP; P01233; 1XUL.
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHb; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 SQ SEQUENCE 165 AA; 17743 MW; 2F21566B48592471 CRC64;

Query Match 76.7%; Score 66; DB 6; Length 165;
 Best Local Similarity 76.5%; Pred. No. 0.0033;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
 Db 61 MMRVLQAVLPVPVQVVC 77
 ||||| ||| :|||||

RESULT 19

Q8WNB6 PRELIMINARY; PRT; 136 AA.

AC Q8WNB6;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Luteinizing hormone beta subunit (Fragment).
 GN LHB.
 OS Presbytis obscura.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; Colobinae;
 OC Presbytis.
 OX NCBI_TaxID=78450;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397594; AAL69722.1; -;
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHb; 1.

DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 136
 SQ SEQUENCE 136 AA; 14722 MW; 2EA6300910968492 CRC64;

Query Match 75.6%; Score 65; DB 6; Length 136;
 Best Local Similarity 86.7%; Pred. No. 0.004;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVLQGVLPALPQVVC 17
 Db 58 RVLQAVLPPLPQVVC 72
 ||||| ||| :|||||

RESULT 20

Q8WNA6 PRELIMINARY; PRT; 156 AA.

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AC Q8WNA6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Aotus trivirgatus (Night monkey) (Douroucoul).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=9505;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
RT evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397604; AAL69732.1; -.
DR InterPro; IPR000359; Cys_knot.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 156
SQ SEQUENCE 156 AA; 16870 MW; 7799AAA1540EA9A7 CRC64;

Query Match 73.3%; Score 63; DB 6; Length 156;
Best Local Similarity 70.6%; Pred. No. 0.0098;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
| |||| | : |||| |
Db 56 MVRVLQTVLPPLPQVVC 72

RESULT 21
Q8WNA7
ID Q8WNA7 PRELIMINARY; PRT; 156 AA.
AC Q8WNA7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Callicebus moloch (Dusky titi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Callicebinae;
OC Callicebus.
OX NCBI_TaxID=9523;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
RT evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397603; AAL69731.1; -.
DR InterPro; IPR000359; Cys_knot.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 156
SQ SEQUENCE 156 AA; 16578 MW; 6EFBD96B513EABE8 CRC64;

Query Match 72.1%; Score 62; DB 6; Length 156;
Best Local Similarity 76.5%; Pred. No. 0.014;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

AY 1 MTRVLQGVLPALPQVVC 17
| |||| | : |||| |
```

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Db 56 MVRVLQTVLPPLPQVVC 72

RESULT 22
Q8WNC3
ID Q8WNC3 PRELIMINARY; PRT; 157 AA.
AC Q8WNC3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Presbytis obscura.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Presbytis.
OX NCBI_TaxID=78450;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
RT evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397586; AAL69714.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 16821 MW; E854A1192407AD0F CRC64;

Query Match 72.1%; Score 62; DB 6; Length 157;
Best Local Similarity 70.6%; Pred. No. 0.014;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
| |||| | : |||| |
Db 56 MMRVLQAVLPVPQAVC 72

RESULT 23
Q8WNC1
ID Q8WNC1 PRELIMINARY; PRT; 157 AA.
AC Q8WNC1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Presbytis obscura.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Presbytis.
OX NCBI_TaxID=78450;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
RT evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397588; AAL69716.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 16745 MW; 1D49080831C14F0C CRC64;
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Query Match 72.1%; Score 62; DB 6; Length 157;
 Best Local Similarity 70.6%; Pred. No. 0.014;
 Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
 | | | | | | | | | | | | | | | | | | | | | |
 Db 56 MMRVLQAVLPVPQAVC 72

RESULT 24

Q8WNB4 Q8WNB4 PRELIMINARY; PRT; 159 AA.
 AC Q8WNB4;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Chorionic gonadotropin beta subunit (Fragment).
 GN CGB.
 OS Colobus guereza (Black-and-white colobus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae;
 OC Colobus.
 OX NCBI_TaxID=33548;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397596; AAL69724.1; -;
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHB; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 159
 SQ SEQUENCE 159 AA; 16904 MW; 71C31ADD81986B01 CRC64;

Query Match 72.1%; Score 62; DB 6; Length 159;
 Best Local Similarity 70.6%; Pred. No. 0.015;
 Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
 | | | | | | | | | | | | | | | | | | | | | |
 Db 56 MMRVLQAVLPVPQAVC 72

RESULT 25

Q8WNB2 Q8WNB2 PRELIMINARY; PRT; 159 AA.
 AC Q8WNB2;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Chorionic gonadotropin beta subunit (Fragment).
 GN CGB.
 OS Colobus guereza (Black-and-white colobus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae;
 OC Colobus.
 OX NCBI_TaxID=33548;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397596; AAL69726.1; -;
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.

DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHB; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 159
 SQ SEQUENCE 159 AA; 16972 MW; 725BA76BC2887660 CRC64;
 Query Match 72.1%; Score 62; DB 6; Length 159;
 Best Local Similarity 70.6%; Pred. No. 0.015;
 Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTRVLQGVLPALPQVVC 17
 | | | | | | | | | | | | | | | | | | | | | |
 Db 56 MMRVLQAVLPVPQAVC 72

Search completed: December 4, 2002, 11:28:32
 Job time : 31.175 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:21:04 ; Search time 28.925 Seconds
(without alignments)
59.888 Million cell updates/sec

Title: US-09-821-380-2
Perfect score: 67
Sequence: 1 LGVLPAIPQVVC 13
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database :

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23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	100.0	13	AAW47477	Human beta-hCG pro
2	67	100.0	13	AAW50037	Human chorionic go
3	67	100.0	13	AAW50072	Human chorionic go
4	67	100.0	13	AAU08737	Human immunoregula
5	67	100.0	13	AAU08737	Beta-human chorion
6	67	100.0	13	AAU08737	Human Satellin A1
7	67	100.0	13	AAU08737	Human beta-hCG pro
8	67	100.0	14	AAW47489	Human beta-hCG pro
9	67	100.0	14	AAW47489	Human beta-hCG pro
10	67	100.0	14	AAW50043	Human chorionic go

11	67	100.0	14	AAW50092	Human chorionic go
12	67	100.0	14	AAW50084	Human chorionic go
13	67	100.0	14	AAW50078	Human chorionic go
14	67	100.0	14	AAW50049	Human chorionic go
15	67	100.0	14	AAW50057	Human chorionic go
16	67	100.0	14	AAW50057	Beta-human chorion
17	67	100.0	14	AAW50057	Beta-hCG Satellin
18	67	100.0	14	AAW50057	Human Satellin A2
19	67	100.0	14	AAW50057	Chorionic gonadotr
20	67	100.0	17	AAW50057	Human immunoregula
21	67	100.0	20	AAW50057	38-57 region of hu
22	67	100.0	20	AAW50057	Peptide similar to
23	67	100.0	20	AAW50057	HCG antigenic pept
24	67	100.0	20	AAW50057	Human hCG beta-sub
25	67	100.0	20	AAW50057	Human chorionic go
26	67	100.0	20	AAW50057	Peptide containing
27	67	100.0	20	AAW50057	Human chorionic go
28	67	100.0	20	AAW50057	Human chorionic go
29	67	100.0	20	AAW50057	Human chorionic go
30	67	100.0	20	AAW50057	Structure XXVII (p
31	67	100.0	22	AAW50057	Human chorionic go
32	67	100.0	22	AAW50057	Sequence of fragme
33	67	100.0	23	AAW50057	Human beta-hCG pro
34	67	100.0	23	AAW50057	Human chorionic go
35	67	100.0	23	AAW50057	Human beta-hCG pro
36	67	100.0	24	AAW50057	Human chorionic go
37	67	100.0	24	AAW50057	Human Clara cell p
38	67	100.0	24	AAW50057	Human Clara cell p
39	67	100.0	25	AAW50057	Human chorionic go
40	67	100.0	27	AAW50057	Human chorionic go
41	67	100.0	60	AAW50057	Beta subunit of hu
42	67	100.0	85	AAW50057	Human chorionic go
43	67	100.0	93	AAW50057	Human chorionic go
44	67	100.0	111	AAW50057	Human chorionic go
45	67	100.0	112	AAW50057	hCG deletion mutan
46	67	100.0	114	AAW50057	Modified hCG beta-
47	67	100.0	114	AAW50057	HCG analogue-G bet
48	67	100.0	114	AAW50057	HCG analogue-Q bet
49	67	100.0	114	AAW50057	HCG analogue-Q bet
50	67	100.0	114	AAW50057	Human chorionic go
51	67	100.0	114	AAW50057	hCG/hfsh chimera,
52	67	100.0	114	AAW50057	hCG/hfsh chimera,
53	67	100.0	115	AAW50057	hCG/hfsh chimera,
54	67	100.0	115	AAW50057	hCG deletion mutan
55	67	100.0	115	AAW50057	hCG methionine sub
56	67	100.0	116	AAW50057	Modified hCG beta-
57	67	100.0	116	AAW50057	Modified hCG beta-
58	67	100.0	117	AAW50057	Modified hCG beta-
59	67	100.0	117	AAW50057	HCG analogue-DGT be
60	67	100.0	117	AAW50057	HCG analogue-DGT be
61	67	100.0	117	AAW50057	hCG/hfsh chimera,
62	67	100.0	118	AAW50057	hCG/hfsh chimera,
63	67	100.0	118	AAW50057	hCG/buH chimera, D
64	67	100.0	122	AAW50057	
65	67	100.0	122	AAW50057	

ALIGNMENTS

RESULT 1
ID AAW47477 standard; Protein; 13 AA.
XX
AC AAW47477;
DT
DT 23-SRP-1998 (first entry)
XX
DE Human beta-hCG protein fragment (aa 45-57).
XX
KW Beta-human chorionic gonadotropin; beta-hCG; hematopoiesic cell;
KW treatment; proliferation; human immunodeficiency virus; HIV; tumour;
KW idiopathic thrombocytopenia purpura; anaemia; neutropaenia;

Wed Dec 4 11:39:36 2002

chemotherapy; radiation; autoimmune disease; genetic disorder.

XX OS Homo sapiens.

XX PN WO9749418-A1.

XX PD 31-DEC-1997.

XX PF 24-JUN-1997; 97WO-US11209.

XX PR 09-SEP-1996; 96US-0709924.

XX PR 24-JUN-1996; 96US-0669654.

XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX PI Bryant J, Gallo RC, Lunardi-Iskandar Y;

XX DR WPI; 1998-076906/07.

XX XX Treating or preventing disease by increasing production of

PT haematopoietic cells - using human chorionic gonadotropin or its

PT fragments or derivatives, in vivo or in vitro, e.g. in cases of HIV

PT infection, anaemia etc.

XX XX Claim 7; Page 92; 162pp; English.

XX XX AAW47474-W47508 represent fragments of the beta subunit of human

CC chorionic gonadotropin which is used in a method for the treatment or

CC prevention of disease, by increasing production of at least one type of

CC haematopoietic cell. A method is also described in which non-terminally

CC differentiated haematopoietic cells are treated in vitro to increase

CC proliferation then returned to the patient. The method is specified for

CC treating human immunodeficiency virus (HIV) infection, idiopathic

CC thrombocytopenia purpura, anaemia or neutropenia, or subjects who have

CC undergone chemotherapy or radiation treatment. More generally it can be

CC used to treat a wide range of conditions involving haematopoietic

CC failure, (non-) haematopoietic tumours, autoimmune disease and genetic

CC disorders (using a transformed haematopoietic cell). The in vitro method

CC can also be used to expand haematopoietic cells for subsequent

CC therapeutic use.

XX XX Sequence 13 AA:

XX Query Match 100.0%; Score 67; DB 19; Length 13;

XX Best Local Similarity 100.0%; Pred. No. 0.00016;

XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13

DB 1 LOGVLPALPQVVC 13

RESULT 2

AAW50037

ID AAW50037 standard; peptide; 13 AA.

XX AC AAW50037;

XX XX 26-JUN-1998 (first entry)

XX XX Human chorionic gonadotropin beta-chain fragment.

XX DE Beta-chain; human; chorionic gonadotropin; beta-hCG; inhibition;

XX KW human immunodeficiency virus; HIV; infection; replication;

XX KW Kaposi's sarcoma; haematopoiesis.

XX OS Homo sapiens.

XX XX WO9749373-A2.

XX XX 31-DEC-1997.

XX XX 24-JUN-1997; 97WO-US11202.

XX PR 09-SEP-1996; 96US-0709948.

XX PR 24-JUN-1996; 96US-0669681.

XX XX (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX PI Bryant J, Gallo RC, Lunardi-Iskandar Y;

XX DR WPI; 1998-076887/07.

XX XX Human chorionic gonadotropin peptide derivatives - are active in

PT inhibiting, e.g. HIV infection or replication, Kaposi's Sarcoma or

PT have pro-haematopoietic activity

XX XX Claim 6; Page 103; 174pp; English.

XX XX The present sequence is a peptide derivative of the beta-chain of

CC human chorionic gonadotropin (beta-hCG). The peptide is active in

CC inhibiting, e.g. HIV infection or replication or Kaposi's sarcoma,

CC or has pro-haematopoietic activity.

XX XX Sequence 13 AA:

XX Query Match 100.0%; Score 67; DB 19; Length 13;

XX Best Local Similarity 100.0%; Pred. No. 0.00016;

XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13

DB 1 LOGVLPALPQVVC 13

RESULT 3

AAW50072

ID AAW50072 standard; peptide; 13 AA.

XX AC AAW50072;

XX XX 26-JUN-1998 (first entry)

XX XX Human chorionic gonadotropin beta-chain fragment.

XX DE Beta-chain; human; chorionic gonadotropin; beta-hCG; treatment;

XX KW prevention; wasting syndrome; viral infection; cancer;

XX KW chronic cardiovascular disease; chemotherapy;

XX KW radiation therapy.

XX OS Homo sapiens.

XX XX WO9749721-A1.

XX XX 31-DEC-1997.

XX XX 24-JUN-1997; 97WO-US11448.

XX XX 09-SEP-1996; 96US-0709933.

XX PR 24-JUN-1996; 96US-0669675.

XX XX (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX PI Bryant J, Gallo RC, Lunardi-Iskandar Y;

XX DR WPI; 1998-077106/07.

XX XX Treating or preventing wasting syndrome - by administration of human

PT chorionic gonadotropin, beta-hCG, peptides or derivatives of these

XX XX Claim 8; Page 71; 126pp; English.

XX XX The present sequence is a peptide derivative of the beta-chain of

CC human chorionic gonadotropin (beta-hCG). The peptide can be used

CC to treat or prevent a wasting syndrome associated with viral

CC infection, e.g. human immunodeficiency syndrome virus infection,

CC cancer, chronic cardiovascular disease, chemotherapy or radiation
 CC therapy.

XX Sequence 13 AA;

Query Match 100.0%; Score 67; DB 19; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQGVLPALPQVVC 13
 |||||
 Db 1 LQGVLPALPQVVC 13

RESULT 4

AAU08737
 ID AAU08737 standard; Peptide; 13 AA.

XX AC AAU08737;

XX DT 19-DEC-2001 (first entry)

XX DE Human immunoregulator functional fragment peptide #2.

XX KW Immunoregulator; human; beta-human chorionic gonadotropin; beta-HCG;
 KW inflammation; multiple sclerosis; diabetes; anaphylactic shock; asthma;
 KW pregnancy related disorder; pre-eclampsia; autoimmune disease; allergy;
 KW rheumatoid arthritis; Sjogren's syndrome; graft-versus-host disease;
 KW thrombocytopenia; pernicious anaemia; Addison's disease; dermatomyositis;
 KW idiopathic leucopenia; primary biliary cirrhosis; cryptogenic cirrhosis;
 KW active chronic hepatitis; ulcerative colitis; polymyositis; scleroderma;
 KW mixed connective tissue disease; discoid lupus erythematosus; neutropenic
 KW antidiabetic; immunosuppressive; dermatological; antirheumatic; virucide;
 KW antiarthritic; antiasthmatic; anti-infertility; haemostatic;
 KW antiinflammatory.

XX OS Homo sapiens.

XX PN EP1138692-A1.

XX PD 04-OCT-2001.

XX PF 29-MAR-2000; 2000EP-0201139.

XX PR 29-MAR-2000; 2000EP-0201139.

XX PA (UYRO-) UNIV ROTTERDAM ERASMUS.

XX PI Khan NA, Benner R;

XX DR WPI; 2001-627804/73.

XX CC Immunoregulator useful in the treatment of e.g. diabetes is obtained or
 CC derived from nicked beta-human chorionic gonadotropin -

XX PS Claim 6; Page 18; 36pp; English.

XX CC The invention relates to an immunoregulator obtained or derived from
 CC nicked beta-human chorionic gonadotropin (beta-HCG). The immunoregulator
 CC can be used in the treatment of immune-mediated disorders such as chronic
 CC inflammation (e.g. multiple sclerosis, diabetes), acute inflammation
 CC (e.g. septic or anaphylactic shock), pregnancy related immune-mediated
 CC disorders (e.g. pre-eclampsia), autoimmune disease (e.g. rheumatoid
 CC arthritis), allergy (e.g. asthma), Sjogren's syndrome, graft-versus-host
 CC disease, thrombocytopenia, pernicious anaemia, Addison's disease,
 CC idiopathic leucopenia, primary biliary cirrhosis, active chronic
 CC hepatitis, cryptogenic cirrhosis, ulcerative colitis, dermatomyositis,
 CC polymyositis, scleroderma, mixed connective tissue disease and discoid
 CC lupus erythematosus. This sequence represents a human immunoregulator
 CC functional fragment peptide.

XX SQ Sequence 13 AA;

Qy 1 LQGVLPALPQVVC 13

Db 1 LQGVLPALPQVVC 13

Query Match 100.0%; Score 67; DB 22; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00016;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQGVLPALPQVVC 13

Db 1 LQGVLPALPQVVC 13

RESULT 5

AAAB71783

ID AAB71783 standard; peptide; 13 AA.

XX AC AAB71783;

XX DT 02-MAY-2001 (first entry)

XX DE Beta-human chorionic gonadotropin Satellin A1 branched peptide.

XX KW Beta-human chorionic gonadotropin; beta-HCG; anti-HIV; cytostatic;
 KW antianaemic; vascular; osteopathic; antiinflammatory; gene therapy;
 KW maternin; MA peptide; pMA peptide; human immunodeficiency virus;
 KW HIV; cancer; wasting disorder; haematopoietic disorder; inflammation;
 KW angiogenic disorder.

XX OS Homo sapiens.

XX PN WO200110907-A2.

XX PD 15-FEB-2001.

XX PF 05-AUG-2000; 2000WO-US21495.

XX PR 06-AUG-1999; 99US-0147825.

XX PR 13-MAR-2000; 2000US-0188777.

XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX PI Gallo R, Bryant J, Lunardi-Iskandar Y, Powell R, Reitz M;

XX PI Foulke J, Lewis G;

XX DR WPI; 2001-147510/15.

XX CC Cells that produce therapeutic beta-human chorionic gonadotropin
 CC fragments, useful for the treatment of human immunodeficiency virus
 CC infections, cancers, wasting disorders, hematopoietic disorders,
 CC inflammation and angiogenic disorders -

XX PS Disclosure; Page 25; 185pp; English.

XX CC The present sequence is given in a specification relating to
 CC therapeutic polypeptides originally isolated from human early pregnancy
 CC urine, now synthetically produced, as well as functional equivalents of
 CC these polypeptides. Novel beta-human chorionic gonadotropin (hCG)
 CC fragments, designated Maternin (RTM) and referred to as MA and pMA
 CC peptides, are disclosed. Both native and synthetic MA inhibited growth
 CC of human tumour cells implanted into immuno-deficient mice by between 60
 CC to 100%, relative to control studies. The therapeutic MA polypeptides
 CC may be used for the prevention and treatment of a range of diseases and
 CC disorders, including human immunodeficiency virus (HIV) infections,
 CC cancers (especially Kaposi's sarcoma), wasting disorders, haematopoietic
 CC disorders (e.g. anaemias, radiation mediated bone marrow damage and
 CC trauma related blood loss), inflammation and angiogenic disorders.

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 67; DB 22; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00016;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQGVLPALPQVVC 13

Db 1 LQGVLPALPQVVC 13

```

XX AC AAW47489;
XX DT 23-SEP-1998 (first entry)
XX DE Human beta-hCG protein fragment (aa 45-58).
XX KW Beta-human chorionic gonadotropin; beta-hCG; hematopoiesic cell;
XX KW treatment; proliferation; human immunodeficiency virus; HIV; tumour;
XX KW idiopathic thrombocytopenia purpura; anaemia; neutropaenia;
XX KW chemotherapy; radiation; autoimmune disease; genetic disorder.
XX OS Homo sapiens.
XX PN WO9749418-A1.
XX PD 31-DEC-1997.
XX PF 24-JUN-1997; 97WO-US11209.
XX PR 09-SEP-1996; 96US-0709924.
XX PR 24-JUN-1996; 96US-0669654.
XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX PI Bryant J, Gallo RC, Lunardi-Iskandar Y;
XX WPI; 1998-076906/07.
XX DR Treating or preventing disease by increasing production of
XX PT haematopoietic cells - using human chorionic gonadotropin or its
XX PT fragments or derivatives, in vivo or in vitro, e.g. in cases of HIV
XX PT infection, anaemia etc.
XX PS Claim 7; Page 95; 162pp; English.
XX CC AAW47474-W47508 represent fragments of the beta subunit of human
XX CC chorionic gonadotropin which is used in a method for the treatment or
XX CC prevention of disease, by increasing production of at least one type of
XX CC haematopoietic cell. A method is also described in which non-terminally
XX CC differentiated haematopoietic cells are treated in vitro to increase
XX CC proliferation then returned to the patient. The method is specified for
XX CC treating human immunodeficiency virus (HIV) infection, idiopathic
XX CC thrombocytopenia purpura, anaemia or neutropaenia, or subjects who have
XX CC undergone chemotherapy or radiation treatment. More generally it can be
XX CC used to treat a wide range of conditions involving haematopoietic
XX CC failure, (non-) haematopoietic tumours, autoimmune disease and genetic
XX CC disorders (using a transformed haematopoietic cell). The in vitro method
XX CC can also be used to expand haematopoietic cells for subsequent
XX CC therapeutic use.
XX SQ Sequence 14 AA;
XX Query Match 100.0%; Score 67; DB 19; Length 14;
XX Best Local Similarity 100.0%; Pred. No. 0.00017;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 LQGVLPALPQVVC 13
XX Db | | | | | | | | | |
XX 1 LQGVLPALPQVVC 13
XX Db | | | | | | | | | |
XX RESULT 8
XX AAW47497
XX ID AAW47497 standard; Protein; 14 AA.
XX AC AAW47497;
XX XX 23-SEP-1998 (first entry)
XX DT Human beta-hCG protein fragment (aa 44-57).
XX DE Beta-human chorionic gonadotropin; beta-hCG; hematopoiesic cell; HIV;
XX KW

XX AC AAW47489;
XX DT 23-SEP-1998 (first entry)
XX DE Human Satellin A1 (SAT_A1) peptide.
XX KW Beta-human chorionic gonadotropin; beta-hCG; luteinising hormone; MA;
XX KW Maternin; human immunodeficiency virus; cancer; brain; breast; pancreas;
XX KW prostate; lung; kidney; haematopoietic malignancy; Kaposi's sarcoma; dog;
XX KW body cell mass; pathological angiogenesis; bacterial infection; anaemia;
XX KW chronic diarrhoea; autoimmune disease; rheumatoid arthritis; diabetes;
XX KW chronic hepatitis; systemic lupus erythematosus; inflammation; cornea;
XX KW osteoporosis; parasitic infection; fungal infection; wound; burn; human;
XX KW horse; sheep; pig; cat; rat; Satellin; lutropin; HIV.
XX OS Homo sapiens.
XX PN WO200111048-A2.
XX PD 15-FEB-2001.
XX PF 05-AUG-2000; 2000WO-US21499.
XX PR 06-AUG-1999; 99US-147825P.
XX PR 13-MAR-2000; 2000US-188777P.
XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX PI Gallo R, Bryant J, Lunardi-Iskandar Y;
XX WPI; 2002-130122/17.
XX DR New therapeutic MA polypeptides corresponding to human chorionic
XX PT gonadotropin peptides, useful for treating and preventing cancers,
XX PT pathological angiogenesis and loss of body cell mass -
XX PS Disclosure; Page 4; 209pp; English.
XX CC The invention relates to Maternin (MA) therapeutic polypeptides and other
XX CC sequences derived from beta-human chorionic gonadotropin (beta-hCG) used
XX CC for treating and/or preventing various medical conditions. The sequences
XX CC are useful for inhibiting HIV replication and for the treatment and
XX CC prevention of human immunodeficiency virus (HIV) infection, cancer (e.g.
XX CC of the brain, breast, lung, pancreas, prostate or kidney), haematopoietic
XX CC malignancy, preferably Kaposi's sarcoma, conditions characterised by loss
XX CC of body cell mass, conditions associated with pathological angiogenesis,
XX CC bacterial infections, chronic diarrhoea, anaemia, autoimmune disease,
XX CC rheumatoid arthritis, diabetes, chronic hepatitis, systemic lupus
XX CC erythematosus, wounds, burns, inflammation (especially of the cornea),
XX CC osteoporosis, parasitic infections and fungal infections. Sequences
XX CC AAW83014-AW83063 represent therapeutic peptides and antigenic peptides
XX CC of the invention.
XX SQ Sequence 13 AA;
XX Query Match 100.0%; Score 67; DB 23; Length 13;
XX Best Local Similarity 100.0%; Pred. No. 0.00016;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 LQGVLPALPQVVC 13
XX Db | | | | | | | | | |
XX 1 LQGVLPALPQVVC 13
XX Db | | | | | | | | | |
XX RESULT 7
XX AAW47489
XX ID AAW47489 standard; Protein; 14 AA.

```

KW treatment; proliferation; human immunodeficiency virus; disulphide;
 KW idiopathic thrombocytopenia purpura; anaemia; neutropaenia; tumour;
 KW chemotherapy; radiation; autoimmune disease; genetic disorder.

XS Homo sapiens.

OS Key Location/Qualifiers

FT Disulfide-bond 1..14

XX XX

PN WO9749418-A1.

XX 31-DEC-1997.

PD 24-JUN-1997; 97WO-US11209.

XX 09-SEP-1996; 96US-0709924.

PR 24-JUN-1996; 96US-0669654.

XX (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX Bryant J, Gallo RC, Lunardi-Iskandar Y;

XX WPI; 1998-076906/07.

DR Treating or preventing disease by increasing production of

XX haematopoietic cells - using human chorionic gonadotropin or its

PT fragments or derivatives, in vivo or in vitro, e.g. in cases of HIV

PT infection, anaemia etc.

XX Claim 7; Page 98; 162pp; English.

XX AAW47474-W47508 represent fragments of the beta subunit of human

CC chorionic gonadotropin which is used in a method for the treatment or

CC prevention of disease, by increasing production of at least one type of

CC haematopoietic cell. A method is also described in which non-terminally

CC differentiated haematopoietic cells are treated in vitro to increase

CC proliferation then returned to the patient. The method is specified for

CC treating human immunodeficiency virus (HIV) infection, idiopathic

CC thrombocytopenia purpura, anaemia or neutropaenia, or subjects who have

CC undergone chemotherapy or radiation treatment. More generally it can be

CC used to treat a wide range of conditions involving haematopoietic

CC failure, (non-) haematopoietic tumours, autoimmune disease and genetic

CC disorders (using a transformed haematopoietic cell). The in vitro method

CC can also be used to expand haematopoietic cells for subsequent

CC therapeutic use.

XX SQ Sequence . 14 AA;

Query Match 100.0%; Score 67; DB 19; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPOVVC 13

DB 2 LOGVLPALPOVVC 14

RESULT 9

AAW47483

ID AAW47483 standard; Protein; 14 AA.

XX AAW47483;

XX 23-SEP-1998 (first entry)

DT Human beta-hCG protein fragment (aa 44-57).

DE Beta-human chorionic gonadotropin; beta-hCG; hematopoiesic cell;

XX treatment; proliferation; human immunodeficiency virus; HIV; tumour;

KW idiopathic thrombocytopenia purpura; anaemia; neutropaenia;

KW chemotherapy; radiation; autoimmune disease; genetic disorder.

XX OS Homo sapiens.

XX WO9749418-A1.

PN 31-DEC-1997.

PD 24-JUN-1997; 97WO-US11209.

XX 09-SEP-1996; 96US-0709924.

PR 24-JUN-1996; 96US-0669654.

XX (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX Bryant J, Gallo RC, Lunardi-Iskandar Y;

XX WPI; 1998-076906/07.

DR Treating or preventing disease by increasing production of

XX haematopoietic cells - using human chorionic gonadotropin or its

PT fragments or derivatives, in vivo or in vitro, e.g. in cases of HIV

PT infection, anaemia etc.

XX Claim 7; Page 94; 162pp; English.

XX AAW47474-W47508 represent fragments of the beta subunit of human

CC chorionic gonadotropin which is used in a method for the treatment or

CC prevention of disease, by increasing production of at least one type of

CC haematopoietic cell. A method is also described in which non-terminally

CC differentiated haematopoietic cells are treated in vitro to increase

CC proliferation then returned to the patient. The method is specified for

CC treating human immunodeficiency virus (HIV) infection, idiopathic

CC thrombocytopenia purpura, anaemia or neutropaenia, or subjects who have

CC undergone chemotherapy or radiation treatment. More generally it can be

CC used to treat a wide range of conditions involving haematopoietic

CC failure, (non-) haematopoietic tumours, autoimmune disease and genetic

CC disorders (using a transformed haematopoietic cell). The in vitro method

CC can also be used to expand haematopoietic cells for subsequent

CC therapeutic use.

XX SQ Sequence 14 AA;

Query Match 100.0%; Score 67; DB 19; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.00017;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPOVVC 13

DB 2 LOGVLPALPOVVC 14

RESULT 10

AAW50043

ID AAW50043 standard; peptide; 14 AA.

XX AAW50043;

XX 26-JUN-1998 (first entry)

DT Human chorionic gonadotropin beta-chain fragment.

DE Beta-chain; human; chorionic gonadotropin; beta-hCG; inhibition;

XX human immunodeficiency virus; HIV; infection; replication;

KW Kaposi's sarcoma; haematopoiesis.

XX OS Homo sapiens.

XX WO9749373-A2.

PN 31-DEC-1997.

XX 24-JUN-1997; 97WO-US11202.

XX 09-SEP-1996; 96US-0709948.

XX 24-JUN-1996; 96US-0669681.

XX DE Human chorionic gonadotrophin beta-chain fragment.
 XX KW Beta-chain; human; chorionic gonadotrophin; beta-hCG; treatment;
 KW prevention; wasting syndrome; viral infection; cancer;
 KW chronic cardiovascular disease; chemotherapy;
 XX radiation therapy.
 XX OS Homo sapiens.
 XX PN WO9749721-A1.
 XX PD 31-DEC-1997.
 XX PF 24-JUN-1997; 97WO-US11448.
 XX PR 09-SEP-1996; 96US-0709933.
 XX PR 24-JUN-1996; 96US-0669675.
 XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 XX PI Bryant J, Gallo RC, Lunardi-Iskandar Y;
 XX WPI; 1998-077106/07.
 XX PT Treating or preventing wasting syndrome - by administration of human
 PT chorionic gonadotrophin, beta-hCG, peptides or derivatives of these
 XX Claim 8; Page 73; 126pp; English.
 XX CC The present sequence is a peptide derivative of the beta-chain of
 CC human chorionic gonadotrophin (beta-hCG). The peptide can be used
 CC to treat or prevent a wasting syndrome associated with viral
 CC infection, e.g. human immunodeficiency syndrome virus infection,
 CC cancer, chronic cardiovascular disease, chemotherapy or radiation
 CC therapy.
 XX SQ Sequence 14 AA;
 XX DE Human chorionic gonadotrophin beta-chain fragment.
 XX KW Beta-chain; human; chorionic gonadotrophin; beta-hCG; inhibition;
 KW human immunodeficiency virus; HIV; infection; replication;
 KW Kaposi's sarcoma; haematopoiesis.
 XX OS Homo sapiens.
 XX PN WO9749373-A2.
 XX PD 31-DEC-1997.
 XX PF 24-JUN-1997; 97WO-US11202.
 XX PR 09-SEP-1996; 96US-0709948.
 XX PR 24-JUN-1996; 96US-0669681.
 XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 XX PI Bryant J, Gallo RC, Lunardi-Iskandar Y;
 XX WPI; 1998-076887/07.
 XX PT Human chorionic gonadotrophin peptide derivatives - are active in
 PT inhibiting, e.g. HIV infection or replication, Kaposi's Sarcoma or
 PT have pro-haematopoietic activity
 XX Example; Page 109; 174pp; English.
 XX CC The present sequence is a peptide derivative of the beta-chain of
 CC human chorionic gonadotrophin (beta-hCG). The peptide is active in
 CC inhibiting, e.g. HIV infection or replication, Kaposi's sarcoma,
 CC or has pro-haematopoietic activity.
 XX SQ Sequence 14 AA;
 XX DE Human chorionic gonadotrophin beta-chain fragment.
 XX KW Beta-chain; human; chorionic gonadotrophin; beta-hCG; inhibition;
 KW human immunodeficiency virus; HIV; infection; replication;
 KW Kaposi's sarcoma; haematopoiesis.
 XX OS Homo sapiens.
 XX PN WO9749373-A2.
 XX PD 31-DEC-1997.
 XX PF 24-JUN-1997; 97WO-US11202.
 XX PR 09-SEP-1996; 96US-0709948.
 XX PR 24-JUN-1996; 96US-0669681.
 XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 XX PI Bryant J, Gallo RC, Lunardi-Iskandar Y;
 XX WPI; 1998-076887/07.
 XX PT Human chorionic gonadotrophin peptide derivatives - are active in
 PT inhibiting, e.g. HIV infection or replication, Kaposi's Sarcoma or
 PT have pro-haematopoietic activity
 XX Example; Page 109; 174pp; English.
 XX CC The present sequence is a peptide derivative of the beta-chain of
 CC human chorionic gonadotrophin (beta-hCG). The peptide is active in
 CC inhibiting, e.g. HIV infection or replication, Kaposi's sarcoma,
 CC or has pro-haematopoietic activity.
 XX SQ Sequence 14 AA;
 XX DE Human chorionic gonadotrophin beta-chain fragment.
 XX KW Beta-chain; human; chorionic gonadotrophin; beta-hCG; inhibition;
 KW human immunodeficiency virus; HIV; infection; replication;
 KW Kaposi's sarcoma; haematopoiesis.
 XX OS Homo sapiens.
 XX PN WO9749373-A2.
 XX PD 31-DEC-1997.
 XX PF 24-JUN-1997; 97WO-US11202.
 XX PR 09-SEP-1996; 96US-0709948.
 XX PR 24-JUN-1996; 96US-0669681.
 XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 XX PI Bryant J, Gallo RC, Lunardi-Iskandar Y;
 XX WPI; 1998-076887/07.
 XX PT Human chorionic gonadotrophin peptide derivatives - are active in
 PT inhibiting, e.g. HIV infection or replication, Kaposi's Sarcoma or
 PT have pro-haematopoietic activity
 XX Example; Page 109; 174pp; English.
 XX CC The present sequence is a peptide derivative of the beta-chain of
 CC human chorionic gonadotrophin (beta-hCG). The peptide is active in
 CC inhibiting, e.g. HIV infection or replication, Kaposi's sarcoma,
 CC or has pro-haematopoietic activity.
 XX SQ Sequence 14 AA;
 XX DE Human chorionic gonadotrophin beta-chain fragment.
 XX KW Beta-chain; human; chorionic gonadotrophin; beta-hCG; inhibition;
 KW human immunodeficiency virus; HIV; infection; replication;
 KW Kaposi's sarcoma; haematopoiesis.
 XX OS Homo sapiens.
 XX PN WO9749373-A2.
 XX PD 31-DEC-1997.
 XX PF 24-JUN-1997; 97WO-US11202.
 XX PR 09-SEP-1996; 96US-0709948.
 XX PR 24-JUN-1996; 96US-0669681.
 XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 XX PI Bryant J, Gallo RC, Lunardi-Iskandar Y;
 XX WPI; 1998-076887/07.
 XX PT Human chorionic gonadotrophin peptide derivatives - are active in
 PT inhibiting, e.g. HIV infection or replication, Kaposi's Sarcoma or
 PT have pro-haematopoietic activity
 XX Example; Page 109; 174pp; English.
 XX CC The present sequence is a peptide derivative of the beta-chain of
 CC human chorionic gonadotrophin (beta-hCG). The peptide is active in
 CC inhibiting, e.g. HIV infection or replication, Kaposi's sarcoma,
 CC or has pro-haematopoietic activity.
 XX SQ Sequence 14 AA;

PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 XX Bryant J, Gallo RC, Lunardi-Iskandar Y;
 XX WPI; 1998-076887/07.
 XX Human chorionic gonadotrophin peptide derivatives - are active in
 PT inhibiting, e.g. HIV infection or replication, Kaposi's Sarcoma or
 PT have pro-haematopoietic activity
 XX Claim 1; Page 106; 174pp; English.
 XX CC The present sequence is a peptide derivative of the beta-chain of
 CC human chorionic gonadotrophin (beta-hCG). The peptide is active in
 CC inhibiting, e.g. HIV infection or replication, Kaposi's sarcoma,
 CC or has pro-haematopoietic activity.
 XX SQ Sequence 14 AA;

Query Match 100.0%; Score 67; DB 19; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
 |||||
 Db 1 LQGVLPALPQVVC 13

RESULT 15
 AAW50057
 ID AAW50057 standard; peptide; 14 AA.
 AC AAW50057;
 XX 26-JUN-1998 (first entry)

XX Human chorionic gonadotrophin beta-chain fragment.
 KW Beta-chain; human; chorionic gonadotrophin; beta-hCG; inhibition;
 KW human immunodeficiency virus; HIV; infection; replication;
 KW Kaposi's sarcoma; haematopoiesis.
 XX OS Homo sapiens.
 XX PN WO9749373-A2.
 XX PD 31-DEC-1997.
 XX PF 24-JUN-1997; 97WO-US11202.
 XX PR 09-SEP-1996; 96US-0709948.
 XX PR 24-JUN-1996; 96US-0669681.
 XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 XX PI Bryant J, Gallo RC, Lunardi-Iskandar Y;
 XX WPI; 1998-076887/07.
 XX Human chorionic gonadotrophin peptide derivatives - are active in
 PT inhibiting, e.g. HIV infection or replication, Kaposi's Sarcoma or
 PT have pro-haematopoietic activity
 XX Example; Page 109; 174pp; English.
 XX CC The present sequence is a peptide derivative of the beta-chain of
 CC human chorionic gonadotrophin (beta-hCG). The peptide is active in
 CC inhibiting, e.g. HIV infection or replication, Kaposi's sarcoma,
 CC or has pro-haematopoietic activity.
 XX SQ Sequence 14 AA;

Query Match 100.0%; Score 67; DB 19; Length 14;

Wed Dec 4 11:39:36 2002

us-09-821-380-2.rag

Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
| | | | | | | | | |
DB 2 LQGVLPALPQVVC 14

RESULT 16
AAB71784
ID AAB71784 standard; peptide; 14 AA.
XX AC AAB71784;
XX 02-MAY-2001 (first entry)
XX DE Beta-human chorionic gonadotrophin Satellin A2 circularised peptide.
XX KW Beta-human chorionic gonadotrophin; beta-hCG; anti-HIV; cytostatic;
KW antianaemic; vascular; osteopathic; antiinflammatory; gene therapy;
KW Maternin; MA peptide; pMA peptide; human immunodeficiency virus;
KW HIV; cancer; wasting disorder; haematopoietic disorder; inflammation;
KW angiogenic disorder; cyclic; circular.
XX OS Homo sapiens.
XX WO200110907-A2.
XX PN 15-FEB-2001.
XX PD 05-AUG-2000; 2000WO-US21495.
XX PF 06-AUG-1999; 99US-0147825.
XX PR 13-MAR-2000; 2000US-0188777.
XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX PI Gallo R, Bryant J, Lunardi-Iskandar Y, Powell R, Reitz M;
PI Foulke J, Lewis G;
XX WPI; 2001-147510/15.
XX CC Cells that produce therapeutic beta-human chorionic gonadotrophin
PT fragments, useful for the treatment of human immunodeficiency virus
PT infections, cancers, wasting disorders, hematopoietic disorders,
PT inflammation and angiogenic disorders -
XX Disclosure; Page 25; 185pp; English.
XX CC The present sequence is given in a specification relating to
CC therapeutic polypeptides originally isolated from human early pregnancy
CC urine, now synthetically produced, as well as functional equivalents of
CC these polypeptides. Novel beta-human chorionic gonadotrophin (hCG)
CC fragments, designated Maternin (RTM) and referred to as MA and pMA
CC peptides, are disclosed. Both native and synthetic MA inhibited growth
CC of human tumour cells implanted into immuno-deficient mice by between 60
CC to 100%, relative to control studies. The therapeutic MA polypeptides
CC may be used for the prevention and treatment of a range of diseases and
CC disorders, including human immunodeficiency virus (HIV) infections,
CC cancers (especially Kaposi's sarcoma), wasting disorders, haematopoietic
CC disorders (e.g. anaemias, radiation mediated bone marrow damage and
CC trauma related blood loss), inflammation and angiogenic disorders.
XX SQ Sequence 14 AA;
Query Match 100.0%; Score 67; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
| | | | | | | | | |
DB 2 LQGVLPALPQVVC 14

RESULT 17
AAB71804
ID AAB71804 standard; peptide; 14 AA.
XX AC AAB71804;
XX 02-MAY-2001 (first entry)
XX DE Beta-hCG Satellin A2 sequence active peptide.
XX KW Human; beta-human chorionic gonadotrophin; beta-hCG; satellin A2;
KW anti-HIV; cytostatic; antianaemic; vascular; osteopathic;
KW antiinflammatory; gene therapy; maternin; MA peptide; pMA peptide;
KW human immunodeficiency virus; HIV; cancer; wasting disorder;
KW haematopoietic disorder; inflammation; angiogenic disorder.
XX OS Homo sapiens.
XX WO200110907-A2.
XX PN 15-FEB-2001.
XX PD 05-AUG-2000; 2000WO-US21495.
XX PF 06-AUG-1999; 99US-0147825.
XX PR 13-MAR-2000; 2000US-0188777.
XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX PI Gallo R, Bryant J, Lunardi-Iskandar Y, Powell R, Reitz M;
PI Foulke J, Lewis G;
XX WPI; 2001-147510/15.
XX CC Cells that produce therapeutic beta-human chorionic gonadotrophin
PT fragments, useful for the treatment of human immunodeficiency virus
PT infections, cancers, wasting disorders, hematopoietic disorders,
PT inflammation and angiogenic disorders -
XX Example; Page 121; 185pp; English.
XX CC The present sequence is given in a specification relating to
CC therapeutic polypeptides originally isolated from human early pregnancy
CC urine, now synthetically produced, as well as functional equivalents of
CC these polypeptides. Novel beta-human chorionic gonadotrophin (hCG)
CC fragments, designated Maternin (RTM) and referred to as MA and pMA
CC peptides, are disclosed. Both native and synthetic MA inhibited growth
CC of human tumour cells implanted into immuno-deficient mice by between 60
CC to 100%, relative to control studies. The therapeutic MA polypeptides
CC may be used for the prevention and treatment of a range of diseases and
CC disorders, including human immunodeficiency virus (HIV) infections,
CC cancers (especially Kaposi's sarcoma), wasting disorders, haematopoietic
CC disorders (e.g. anaemias, radiation mediated bone marrow damage and
CC trauma related blood loss), inflammation and angiogenic disorders.
XX SQ Sequence 14 AA;
Query Match 100.0%; Score 67; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
| | | | | | | | | |
DB 2 LQGVLPALPQVVC 14

RESULT 18
AAU83033
ID AAU83033 standard; peptide; 14 AA.
XX AC AAU83033;
XX

DT 23-APR-2002 (first entry)
 XX Human Satellite A2 (SAT-A2) peptide.
 DE
 XX Beta-human chorionic gonadotropin; beta-hCG; luteinising hormone; MA;
 KW Maternal; human immunodeficiency virus; cancer; brain; breast; pancreas;
 KW prostate; lung; kidney; haematopoietic malignancy; Kaposi's sarcoma; dog;
 KW body cell mass; pathological angiogenesis; bacterial infection; anaemia;
 KW chronic diarrhoea; autoimmune disease; rheumatoid arthritis; diabetes;
 KW chronic hepatitis; systemic lupus erythematosus; inflammation; cornea;
 KW osteoporosis; parasitic infection; fungal infection; wound; burn; human;
 KW horse; sheep; pig; cat; rat; Satellite; lutropin; HIV.
 XX
 OS Homo sapiens.
 XX
 XX WO200111048-A2.
 PN 15-FEB-2001.
 XX
 PD
 XX 05-AUG-2000; 2000WO-US21499.
 PF
 XX 06-AUG-1999; 99US-147825P.
 PR 13-MAR-2000; 2000US-18877P.
 XX
 XX (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 PA Gallo R, Bryant J, Lunardi-Iskandar Y;
 XX WPI; 2002-130122/17.
 DR
 XX New therapeutic MA polypeptides corresponding to human chorionic
 PT gonadotropin peptides, useful for treating and preventing cancers,
 PT pathological angiogenesis and loss of body cell mass -
 XX Examples; Page 121; 209pp; English.
 PS
 XX The invention relates to Maternin (MA) therapeutic polypeptides and other
 CC sequences derived from beta-human chorionic gonadotropin (beta-hCG) used
 CC for treating and/or preventing various medical conditions. The sequences
 CC are useful for inhibiting HIV replication and for the treatment and
 CC prevention of human immunodeficiency virus (HIV) infection, cancer (e.g.
 CC of the brain, breast, lung, pancreas, prostate or kidney), haematopoietic
 CC malignancy, preferably Kaposi's sarcoma, conditions characterised by loss
 CC of body cell mass, conditions associated with pathological angiogenesis,
 CC bacterial infections, chronic diarrhoea, anaemia, autoimmune disease,
 CC rheumatoid arthritis, diabetes, chronic hepatitis, systemic lupus
 CC erythematosus, wounds, burns, inflammation (especially of the cornea),
 CC osteoporosis, parasitic infections and fungal infections. Sequences
 CC AAU83014-AAU83063 represent therapeutic peptides and antigenic peptides
 CC of the invention.
 XX
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 67; DB 23; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.00017;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LQGVLPALPQVVC 13
 Db 2 LQGVLPALPQVVC 14
 |||||
 RESULT 19
 AAU15308
 ID AAU15308 standard; peptide; 17 AA.
 XX
 AC AAU15308;
 XX
 DT 01-JUL-1997 (first entry)
 XX Chorionic gonadotropin whose release is increased in hypoxia.
 DE
 XX Release; expression; secretion; mammal; foetus; trophoblast; cell;

KW chorionic; villus; increase; hypoxia; marker; indicator; abnormal;
 KW maternal; placental; interface; function; abortion; screening;
 KW intrauterine; growth; retardation; gestation; disease; tumour;
 KW molar; pregnancy; choriocarcinoma; ectopic; gonadotropin;
 KW proteinuria; hypertension; preeclampsia; induction;
 KW gonadotropin; mitigation.
 XX Homo sapiens.
 XX WO9633214-A2.
 PN 24-OCT-1996.
 XX
 PD 18-APR-1996; 96WO-US05441.
 PF
 XX 18-APR-1995; 95US-0423409.
 PR
 XX (REGC) UNIV CALIFORNIA.
 PA Burlingame AL, Clauser KR, Fisher SJ, Foulk R, Genbacev O;
 PI WPI; 1996-497265/49.
 DR
 XX Detection of abnormal placental function or metastases - by
 PT detecting proteins with altered expression or trophoblasts or
 PT chorionic villi under hypoxic conditions
 XX
 PS Claim 1; Page 40; 57pp; English.
 XX
 CC The level of release of the present peptide by a mammalian foetal
 CC trophoblast cell or a chorionic villus is increased when the cell
 CC or villus is grown under hypoxic conditions, characterised by a
 CC partial pressure of oxygen (pO2) of 14 mm Hg. The peptide can be
 CC used as a marker for the presence of hypoxic conditions indicative
 CC of an abnormal maternal-placental interface, and consequent
 CC abnormal placental function in, e.g. threatened abortion,
 CC intrauterine growth retardation, gestational trophoblast diseases
 CC including molar pregnancy, choriocarcinoma, placental site tumours,
 CC ectopic pregnancy, proteinuria, pregnancy induced hypertension and
 CC preeclampsia. It can also be used to screen for inducers or
 CC mitigators of abnormal maternal-placental interface.
 XX
 SQ Sequence 17 AA;
 Query Match 100.0%; Score 67; DB 17; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.00021;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 LQGVLPALPQVVC 13
 Db 2 LQGVLPALPQVVC 14
 |||||
 RESULT 20
 AAU08736
 ID AAU08736 standard; peptide; 17 AA.
 XX
 AC AAU08736;
 XX
 DT 19-DEC-2001 (first entry)
 XX Human immunoregulator functional fragment peptide #1.
 DE
 DE
 XX Immunoregulator; human; beta-human chorionic gonadotropin; beta-HCG;
 KW inflammation; multiple sclerosis; diabetes; anaphylactic shock; asthma;
 KW pregnancy related disorder; pre-eclampsia; autoimmune disease; allergy;
 KW rheumatoid arthritis; Sjogren's syndrome; graft-versus-host disease;
 KW thrombocytopenia; pernicious anaemia; Addison's disease; dermatomyositis;
 KW idiopathic leucopenia; primary biliary cirrhosis; cryptogenic cirrhosis;
 KW active chronic hepatitis; ulcerative colitis; polymyositis; scleroderma;
 KW mixed connective tissue disease; discoid lupus erythematosus; nontropic;
 KW antidiabetic; immunosuppressive; dermatological; antirheumatic; virucide;
 KW antiarthritic; antiasthmatic; anti-infertility; haemostatic;

KW antiinflammatory.
 XX Homo sapiens.
 XX EPI1138692-A1.
 XX 04-OCT-2001.
 XX 29-MAR-2000; 2000EP-0201139.
 XX 29-MAR-2000; 2000EP-0201139.
 XX (UVR0-) UNIV ROTTERDAM ERASMUS.
 XX Khan NA, Benner R;
 XX WPI; 2001-627804/73.
 XX Immunoregulator useful in the treatment of e.g. diabetes is obtained or
 PT derived from nicked beta-human chorionic gonadotropin -
 XX Claim 5; Page 18; 36pp; English.
 XX The invention relates to an immunoregulator obtained or derived from
 CC nicked beta-human chorionic gonadotropin (beta-HCG). The immunoregulator
 CC can be used in the treatment of immune-mediated disorders such as chronic
 CC inflammation (e.g. multiple sclerosis, diabetes), acute inflammation
 CC (e.g. septic or anaphylactic shock), pregnancy related immune-mediated
 CC disorders (e.g. pre-eclampsia), autoimmune disease (e.g. rheumatoid
 CC arthritis), allergy (e.g. asthma), Sjogren's syndrome, graft-versus-host
 CC disease, thrombocytopenia, pernicious anaemia, Addison's disease,
 CC idiopathic leucopenia, primary biliary cirrhosis, active chronic
 CC hepatitis, cryptogenic cirrhosis, ulcerative colitis, dermatomyositis,
 CC polymyositis, scleroderma, mixed connective tissue disease and discoid
 CC lupus erythematosus. This sequence represents a human immunoregulator
 XX functional fragment peptide.
 XX Sequence 17 AA;
 Query Match 100.0%; Score 67; DB 22; Length 17;
 Best Local Similarity 100.0%; Pred. No. 0.00021;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQGVLPALPQVVC 13
 DB 5 LQGVLPALPQVVC 17
 RESULT 21
 AAP91856
 ID AAP91856 standard; peptide; 20 AA.
 XX AAP91856;
 XX 07-MAR-1990 (first entry)
 XX 38-57 region of human chorionic gonadotropin.
 XX Human chorionic gonadotropin; beta-subunit; analogue; antibodies.
 XX Homo sapiens.
 XX US4855285-A.
 XX 08-AUG-1989.
 XX 17-AUG-1987; 87US-0086401.
 XX 04-DEC-1985; 85US-0804642.
 XX 17-AUG-1987; 87US-0086401.
 XX (OHIS) OHIO STATE UNIVERSITY RESEARCH FOUNDATION.
 PA
 XX Stevens VC;
 WPI; 1989-285270/39.
 Controlling biological activity of chorionic gonadotropin - by
 administering a peptide comprising the 38-57 region coupled to material
 to evoke antibodies.
 Claim 9; page 57; 82pp; english.
 The peptide is modified outside the body, eg with diphtheria toxoid, then
 reintroduced into the body to produce an enhanced antibody response to
 the unmodified peptide. The peptide may further comprise a peptide
 sequence similar to part of the 110-145 region of HCG beta-subunit.
 CC When modified with (poly)lysine carrier, a second peptide is also joined,
 CC to increase antigenicity. Used for purpose of contraception, abortion,
 CC treatment of hormone-related diseases and hormone-associated carcinomas,
 CC and to boost resistance, eg to viral proteins.

PI Stevens VC;
 XX WPI; 1989-285270/39.
 XX Controlling biological activity of chorionic gonadotropin
 PT - by administering a peptide comprising the 38-57 region coupled to
 PT material to evoke antibodies.
 XX Disclosure; page 14; 82pp; English.
 XX The peptide is the 38-57 region of human chorionic gonadotropin.
 CC Peptide is coupled to a target material, eg poly(lysine) or diphtheria
 CC or cholera toxoid, epichlorohydrin, etc, and used to form antibodies in
 CC primates which control chorionic gonadotropin activity. When the carrier
 CC is poly(lysine), a second polypeptide is added to increase antigenicity.
 CC The peptide can be used for contraception, abortion, to treat hormone-
 CC related diseases and disorders, hormone-associated carcinoma and to boost
 CC resistance to exogenous, eg viral, proteins.
 XX Sequence 20 AA;
 Query Match 100.0%; Score 67; DB 10; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.00025;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LQGVLPALPQVVC 13
 DB 8 LQGVLPALPQVVC 20
 RESULT 22
 AAP90568
 ID AAP90568 standard; peptide; 20 AA.
 XX AAP90568;
 XX 31-JAN-1990 (first entry)
 XX Peptide similar to the 38-57 region of beta-subunit of human chorionic
 DE gonadotropin.
 XX Human chorionic gonadotropin.
 XX Homo sapiens.
 XX US4855285-A.
 XX 08-AUG-1989.
 XX 17-AUG-1987; 87US-0086401.
 XX 04-DEC-1985; 85US-0804642.
 XX (OHIS) OHIO STATE UNIVERSITY.
 PA
 XX Stevens VC;
 WPI; 1989-285270/39.
 Controlling biological activity of chorionic gonadotropin - by
 administering a peptide comprising the 38-57 region coupled to material
 to evoke antibodies.
 Claim 9; page 57; 82pp; english.
 The peptide is modified outside the body, eg with diphtheria toxoid, then
 reintroduced into the body to produce an enhanced antibody response to
 the unmodified peptide. The peptide may further comprise a peptide
 sequence similar to part of the 110-145 region of HCG beta-subunit.
 CC When modified with (poly)lysine carrier, a second peptide is also joined,
 CC to increase antigenicity. Used for purpose of contraception, abortion,
 CC treatment of hormone-related diseases and hormone-associated carcinomas,
 CC and to boost resistance, eg to viral proteins.

```

XX SQ Sequence 20 AA;
Query Match 100.0%; Score 67; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
DB 8 LQGVLPALPQVVC 20

RESULT 23
AAW69468
ID AAW69468 standard; peptide; 20 AA.
XX AC AAW69468;
XX DT 18-DEC-1998 (first entry)
XX DE HCG antigenic peptide structure (XXVII).
XX Antigenic peptide; HCG; human chorionic gonadotropin; vascular disease;
XX antigenic modification; immunogenic conjugate; vaccine development;
XX anti-pregnancy vaccine; hormone related tumour; endocrine related tumour;
XX cancer; hypertension; angiotensin; diabetes; therapy.
XX Synthetic.
XX OS Homo sapiens.
XX US5817753-A.
XX 06-OCT-1998.
XX 06-OCT-1992; 92US-0958601.
XX 07-AUG-1989; 89US-0390530.
XX 04-DEC-1985; 85US-0804642.
XX 17-AUG-1987; 87US-0086401.
XX 06-OCT-1992; 92US-0958601.
XX (OHIS ) UNIV OHIO STATE. RES FOUND.
XX Stevens VC;
XX WPI; 1998-556460/47.
XX Modified human chorionic gonadotropin beta sub:unit peptide(s) -
XX useful for producing immunogenic conjugates with proteins that are
XX not normally immunogenic, for use as vaccines
XX Disclosure; Column 25; 81pp; English.
XX This sequence represents a synthetic analogue of a human chorionic
XX gonadotropin (hCG) beta subunit, and represents an antigenic peptide of
XX the invention. The peptides are preferably analogues of hCG beta residues
XX 38-57. The invention provides a method for the antigenic modification of
XX peptides. The peptides can then be coupled to carrier proteins,
XX e.g. diphtheria toxoid, to produce immunogenic conjugates that elicit
XX anti-hCG antibodies (but at a lower level than the native peptide) and do
XX not elicit antibodies to human luteinising hormone. The conjugates can be
XX used for vaccine development or to produce polyclonal antisera for
XX diagnostic assays. Depending on the peptides used, the vaccines can be
XX used to treat hormone and endocrine related tumours, cancers,
XX hypertension (especially using angiotensin related peptides), and
XX diabetes and associated vascular diseases, or as anti-pregnancy vaccines
XX (especially post-conception). The adapted peptides allow production of
XX vaccines from endogenous proteins, which are not normally immunogenic.
XX SQ Sequence 20 AA;
Query Match 100.0%; Score 67; DB 19; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
DB 8 LQGVLPALPQVVC 20

RESULT 24
AAW93453
ID AAW93453 standard; peptide; 20 AA.
XX AC AAW93453;
XX DT 11-JUN-1999 (first entry)
XX DE Human hCG beta-subunit peptide structure XXVII.
XX Human chorionic gonadotropin; beta subunit; antigenic peptide; hCG;
XX contraceptive; vaccine; fertility; polyclonal antisera; diagnostic;
XX immunogen; human luteinising hormone.
XX OS Homo sapiens.
XX US5891992-A.
XX 06-APR-1999.
XX 06-JUN-1995; 95US-0467569.
XX 07-AUG-1989; 89US-0390530.
XX 04-DEC-1985; 85US-0804642.
XX 17-AUG-1987; 87US-0086401.
XX 06-OCT-1992; 92US-0958601.
XX 06-JUN-1995; 95US-0467569.
XX (OHIS ) UNIV OHIO STATE RES FOUND.
XX Stevens VC;
XX WPI; 1999-253928/21.
XX Synthetic antigenic peptides from human chorionic gonadotropin
XX beta-subunit
XX Disclosure; Column 25; 80pp; English.
XX This invention describes novel synthetic antigenic peptides (A) based
XX on the human chorionic gonadotropin (hCG) beta-subunit. These peptides
XX have contraceptive properties and are used for the development of
XX vaccines used to control fertility in animals and to generate
XX polyclonal antisera for diagnostic use. The peptides are more specific
XX immunogens than corresponding unmodified peptides from hCG beta-subunit,
XX i.e. they do not elicit antibodies that cross-react with human
XX luteinising hormone.
XX SQ Sequence 20 AA;
Query Match 100.0%; Score 67; DB 20; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
DB 8 LQGVLPALPQVVC 20

RESULT 25
AAB15353
ID AAB15353 standard; peptide; 20 AA.
XX AC AAB15353;
XX DT 15-FEB-2001 (first entry)

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us-09-821-380-2.rag

Wed Dec 4 11:39:36 2002

```

XX Human chorionic gonadotrophin beta-subunit loop peptide.
DE
XX Human; chorionic gonadotrophin; hCG; DNA vaccine; cancer;
KW fertility control; contraceptive; immunogen.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Disulfide-bond 1..20
FT
XX WO200041717-A2.
XX
XX PD 20-JUL-2000.
XX
XX PF 17-DEC-1999; 99WO-US30232.
XX
XX PR 18-DEC-1998; 98US-0112910.
XX
XX PA (AVIB-) AVI BIOPHARMA INC.
XX
XX PI Iversen PL;
XX
XX WPI; 2000-466124/40.
DR N-PSDB; AAA73831.
DR
XX Inducing immune response to human chorionic gonadotropin (hCG), useful
PT for treatment of cancer and fertility control comprises exposing cells
PT to nucleic acid construct encoding hCG immunogenic epitope -
XX
XX Claim 24; Fig 1H; 45pp; English.
XX
XX The present sequence comprises part of the human chorionic
CC gonadotrophin (hCG) beta-subunit, which forms a loop due to the
CC presence of two cysteine residues. It was used in the methods of the
CC invention which involve the use of DNA vaccines encoding hCG antigens
CC to induce an immune response and enable the treatment of cancer and
CC provide a novel method of fertility control. In particular, they can be
CC used to treat colorectal, breast and lung cancer, as hCG is associated
CC with these types of tumours.
XX
SQ Sequence 20 AA;
Query Match 100.0%; Score 67; DB 21; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LQGVLPALPQVVC 13
Db 8 LQGVLPALPQVVC 20
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Search completed: December 4, 2002, 11:26:05
Job time : 28.925 secs

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GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:24:35 ; Search time 11.05 Seconds
(without alignments)
34.615 Million cell updates/sec

Title: US-09-821-380-2
Perfect score: 67
Sequence: 1 LOGVLPALPQVVC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

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2: /cgn2.6/ptodata/1/iaa/5B_COMB.pep: *
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4: /cgn2.6/ptodata/1/iaa/6B_COMB.pep: *
5: /cgn2.6/ptodata/1/iaa/PCTUS_COMB.pep: *
6: /cgn2.6/ptodata/1/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	100.0	13	2	US-08-709-924-6
2	67	100.0	13	2	US-08-709-925-6
3	67	100.0	13	4	US-08-709-948-6
4	67	100.0	14	2	US-08-709-924-12
5	67	100.0	14	2	US-08-709-924-18
6	67	100.0	14	2	US-08-709-924-26
7	67	100.0	14	2	US-08-709-925-12
8	67	100.0	14	2	US-08-709-925-18
9	67	100.0	14	2	US-08-709-925-26
10	67	100.0	14	4	US-08-709-948-12
11	67	100.0	14	4	US-08-709-948-18
12	67	100.0	14	4	US-08-709-948-26
13	67	100.0	93	4	US-08-918-288-70
14	67	100.0	93	4	US-08-918-288-70
15	67	100.0	114	1	US-08-425-673-7
16	67	100.0	114	1	US-08-425-673-7
17	67	100.0	114	1	US-08-425-673-8
18	67	100.0	114	1	US-08-918-288-69
19	67	100.0	114	4	US-08-918-288-69
20	67	100.0	117	1	US-08-425-673-11
21	67	100.0	117	1	US-08-425-673-12
22	67	100.0	145	1	US-08-425-673-1
23	67	100.0	145	1	US-08-425-673-2
24	67	100.0	145	1	US-08-425-673-10
25	67	100.0	145	1	US-08-298-189B-1
26	67	100.0	145	1	US-08-475-213-10
27	67	100.0	145	2	US-08-395-238-2

28	67	100.0	145	4	US-09-142-320-4	Sequence 4, Appli
29	67	100.0	145	4	US-09-142-320-11	Sequence 11, Appl
30	67	100.0	145	4	US-09-142-320-12	Sequence 12, Appl
31	67	100.0	145	4	US-09-142-320-13	Sequence 13, Appl
32	67	100.0	145	4	US-09-142-320-14	Sequence 14, Appl
33	67	100.0	145	4	US-09-142-320-15	Sequence 15, Appl
34	67	100.0	145	4	US-09-142-320-16	Sequence 16, Appl
35	67	100.0	145	4	US-08-918-288-68	Sequence 68, Appl
36	67	100.0	145	4	US-08-918-288-68	Sequence 68, Appl
37	67	100.0	145	4	US-08-908-371B-1	Sequence 1, Appli
38	67	100.0	165	2	US-08-709-924-2	Sequence 2, Appli
39	67	100.0	165	2	US-08-709-925-2	Sequence 2, Appli
40	67	100.0	165	4	US-08-709-948-2	Sequence 2, Appli
41	67	100.0	181	4	US-08-918-288-36	Sequence 36, Appl
42	67	100.0	181	4	US-08-918-288-36	Sequence 36, Appl
43	67	100.0	234	4	US-08-918-288-6	Sequence 6, Appli
44	67	100.0	234	4	US-08-918-288-21	Sequence 21, Appl
45	67	100.0	234	4	US-08-918-288-24	Sequence 24, Appl
46	67	100.0	234	4	US-08-918-288-3	Sequence 3, Appli
47	67	100.0	234	4	US-08-918-288-3	Sequence 3, Appli
48	67	100.0	234	4	US-08-918-288-3	Sequence 3, Appli
49	67	100.0	237	4	US-08-918-288-15	Sequence 15, Appl
50	67	100.0	237	4	US-08-918-288-15	Sequence 15, Appl
51	67	100.0	237	4	US-08-918-288-15	Sequence 15, Appl
52	67	100.0	237	4	US-08-918-288-15	Sequence 15, Appl
53	67	100.0	265	4	US-08-918-288-3	Sequence 3, Appli
54	67	100.0	265	4	US-08-918-288-3	Sequence 3, Appli
55	67	100.0	265	4	US-08-918-288-3	Sequence 3, Appli
56	67	100.0	265	4	US-08-918-288-3	Sequence 3, Appli
57	67	100.0	307	4	US-08-804-166-4	Sequence 4, Appli
58	67	100.0	307	4	US-08-804-166-4	Sequence 4, Appli
59	67	100.0	336	4	US-08-910-991-4	Sequence 4, Appli
60	67	100.0	336	4	US-08-910-991-4	Sequence 4, Appli
61	58	86.6	12	2	US-08-709-924-17	Sequence 17, Appl
62	58	86.6	12	2	US-08-709-924-22	Sequence 22, Appl
63	58	86.6	12	2	US-08-709-925-17	Sequence 17, Appl
64	58	86.6	12	2	US-08-709-925-22	Sequence 22, Appl
65	58	86.6	12	4	US-08-709-948-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-709-924-6
; Sequence 6, Application US/08709924
; Patent No. 5968513
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHODS OF PROMOTING HEMATOPOIESIS
; USING DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,924
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872

Wed Dec 4 11:39:36 2002

us-09-821-380-2.ra1

REFERENCE/DOCKET NUMBER: 8769-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-709-924-6

Query Match 100.0%; Score 67; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
Db 1 LOGVLPALPQVVC 13

RESULT 2
US-08-709-925-6
; Sequence 6, Application US/08709925
; Patent No. 5997871
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF CANCER BY
; ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,925
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 512
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-709-925-6

Query Match 100.0%; Score 67; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
Db 1 LOGVLPALPQVVC 13

RESULT 3
US-08-709-948-6
; Sequence 6, Application US/08709948
; Patent No. 6319504
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HIV INFECTION
; BY ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOT
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,948
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-709-948-6

Query Match 100.0%; Score 67; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
Db 1 LOGVLPALPQVVC 13

RESULT 4
US-08-709-924-12
; Sequence 12, Application US/08709924
; Patent No. 5968513
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHODS OF PROMOTING HEMATOPOIESIS
; USING DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA: US/08/709,924
 ; FILING DATE: 09-SEP-1996
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mirock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 8769-018
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-709-924-12

Query Match 100.0%; Score 67; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
 Db 2 LQGVLPALPQVVC 14

RESULT 5
 US-08-709-924-18
 ; Sequence 18, Application US/08709924
 ; Patent No. 5968513
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallo, Robert C.
 ; APPLICANT: Bryant, Joseph
 ; APPLICANT: Lunardi-Iskandar, Yanto
 ; TITLE OF INVENTION: METHODS OF PROMOTING HEMATOPOIESIS
 ; TITLE OF INVENTION: USING DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; FILING DATE: 09-SEP-1996
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mirock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 8769-018
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 18:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide

US-08-709-924-18

Query Match 100.0%; Score 67; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
 Db 1 LQGVLPALPQVVC 13

RESULT 6
 US-08-709-924-26
 ; Sequence 26, Application US/08709924
 ; Patent No. 5968513
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallo, Robert C.
 ; APPLICANT: Bryant, Joseph
 ; APPLICANT: Lunardi-Iskandar, Yanto
 ; TITLE OF INVENTION: METHODS OF PROMOTING HEMATOPOIESIS
 ; TITLE OF INVENTION: USING DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/709,924
 ; FILING DATE: 09-SEP-1996
 ; CLASSIFICATION: 514
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mirock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 8769-018
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 26:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: peptide
 US-08-709-924-26

Query Match 100.0%; Score 67; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
 Db 2 LQGVLPALPQVVC 14

RESULT 7
 US-08-709-925-12
 ; Sequence 12, Application US/08709925
 ; Patent No. 5997871
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallo, Robert C.
 ; APPLICANT: Bryant, Joseph
 ; APPLICANT: Lunardi-Iskandar, Yanto
 ; TITLE OF INVENTION: TREATMENT AND PREVENTION OF CANCER BY
 ; ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROP

NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,925
FILING DATE: 09-SEP-1996
CLASSIFICATION: 512
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8769-017
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-709-925-12

Query Match 100.0%; Score 67; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
| | | | | | | | | | | | | | | |
Db 2 LQGVLPALPQVVC 14

RESULT 8
US-08-709-925-18
; Sequence 18, Application US/08709925
; Patent No. 5997871
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF CANCER BY
; TITLE OF INVENTION: ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,925
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 512
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-017

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-709-925-18

Query Match 100.0%; Score 67; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
| | | | | | | | | | | | | | | |
Db 1 LQGVLPALPQVVC 13

RESULT 9
US-08-709-925-26
; Sequence 26, Application US/08709925
; Patent No. 5997871
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF CANCER BY
; TITLE OF INVENTION: ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROP
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,925
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 512
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-08-709-925-26

Query Match 100.0%; Score 67; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
| | | | | | | | | | | | | | | |
Db 2 LQGVLPALPQVVC 14


```
RESULT 10
US-08-709-948-12
; Sequence 12, Application US/08709948
; Patent No. 6319504
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HIV INFECTION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,948
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-016
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-709-948-12

Query Match 100.0%; Score 67; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
Db 2 LOGVLPALPQVVC 14

RESULT 11
US-08-709-948-18
; Sequence 18, Application US/08709948
; Patent No. 6319504
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HIV INFECTION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,948
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-016
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-709-948-18

Query Match 100.0%; Score 67; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
Db 1 LOGVLPALPQVVC 13

RESULT 12
US-08-709-948-26
; Sequence 26, Application US/08709948
; Patent No. 6319504
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HIV INFECTION
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,948
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-016
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-08-709-948-26
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Query Match 100.0%; Score 67; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQGVLPALPQVVC 13
Db 2 LQGVLPALPQVVC 14

RESULT 13

US-08-918-288-70
; Sequence 70, Application US/08918288
; Patent No. 6238890
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/918,288
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/282,357
; FILING DATE:
; APPLICATION NUMBER: 08/853,524
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 08/199,382
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20050.25
; TELEPHONE: 202-887-1500
; TELEFAX: 202-887-0763
; TELEX:
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-918-288-70

Query Match 100.0%; Score 67; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQGVLPALPQVVC 13
Db 45 LQGVLPALPQVVC 57

RESULT 14

US-09-282-357-70
; Sequence 70, Application US/09282357
; Patent No. 6242580
; GENERAL INFORMATION:

; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/282,357
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/918,288
; FILING DATE: 25 AUG-1997
; APPLICATION NUMBER: 08/853,524
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 08/199,382
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 29500-20050.25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-887-0763
; TELEX:
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 93 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-282-357-70

Query Match 100.0%; Score 67; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQGVLPALPQVVC 13
Db 45 LQGVLPALPQVVC 57

RESULT 15

US-08-425-673-7
; Sequence 7, Application US/08425673
; Patent No. 5508261
; GENERAL INFORMATION:
; APPLICANT: Moyle, William R.
; APPLICANT: Campbell, Robert K.
; TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
; TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
; TITLE OF INVENTION: Methods For Preparing and Using Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: P.O. Box 1267
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08551
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

[illegible]


```
;; APPLICATION NUMBER: US 07/717,151
;; FILING DATE: 18-JUN-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Muccino, Richard R.
;; REGISTRATION NUMBER: 32,538
;; REFERENCE/DOCKET NUMBER: UMD 1.0-004
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (609) 466-3407
;; TELEFAX: (609) 466-2760
;; INFORMATION FOR SEQ ID NO: 11:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 117 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
US-08-425-673-11

Query Match 100.0%; Score 67; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
Db 45 LQGVLPALPQVVC 57

RESULT 21
US-08-425-673-12
; Sequence 12, Application US/08425673
; Patent No. 5508261
; GENERAL INFORMATION:
; APPLICANT: Moyle, William R.
; TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
; TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
; TITLE OF INVENTION: Methods For Preparing and Using Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: P.O. Box 1267
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08551
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 07/717,151
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/717,151
; FILING DATE: 18-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Muccino, Richard R.
; REGISTRATION NUMBER: 32,538
; REFERENCE/DOCKET NUMBER: UMD 1.0-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 466-3407
; TELEFAX: (609) 466-2760
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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US-08-425-673-12

Query Match 100.0%; Score 67; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
Db 45 LQGVLPALPQVVC 57

RESULT 22
US-08-425-673-1
; Sequence 1, Application US/08425673
; Patent No. 5508261
; GENERAL INFORMATION:
; APPLICANT: Moyle, William R.
; APPLICANT: Campbell, Robert K.
; TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
; TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
; TITLE OF INVENTION: Methods For Preparing and Using Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: P.O. Box 1267
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08551
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,673
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/717,151
; FILING DATE: 18-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Muccino, Richard R.
; REGISTRATION NUMBER: 32,538
; REFERENCE/DOCKET NUMBER: UMD 1.0-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 466-3407
; TELEFAX: (609) 466-2760
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-425-673-1

Query Match 100.0%; Score 67; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
Db 45 LQGVLPALPQVVC 57

RESULT 23
US-08-425-673-2
; Sequence 2, Application US/08425673
; Patent No. 5508261
; GENERAL INFORMATION:
; APPLICANT: Moyle, William R.
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; APPLICANT: Campbell, Robert K.
; TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
; TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
; TITLE OF INVENTION: Methods for Preparing and Using Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: P.O. Box 1267
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08551
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,673
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/717,151
; FILING DATE: 18-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Muccino, Richard R.
; REGISTRATION NUMBER: 32,538
; REFERENCE/DOCKET NUMBER: UMD 1.0-004
; TELEPHONE: (609) 466-3407
; TELEFAX: (609) 466-2760
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-425-673-2

Query Match 100.0%; Score 67; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPOVVC 13
Db 45 LQGVLPALPOVVC 57

RESULT 24
US-08-425-673-10
; Sequence 10, Application US/08425673
; Patent No. 5508261
; GENERAL INFORMATION:
; APPLICANT: Moyle, William R.
; APPLICANT: Campbell, Robert K.
; TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
; TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
; TITLE OF INVENTION: Methods for Preparing and Using Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: P.O. Box 1267
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08551
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,673
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/717,151
; FILING DATE: 18-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Muccino, Richard R.
; REGISTRATION NUMBER: 32,538
; REFERENCE/DOCKET NUMBER: UMD 1.0-004
; TELEPHONE: (609) 466-3407
; TELEFAX: (609) 466-2760
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-425-673-10

Query Match 100.0%; Score 67; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPOVVC 13
Db 45 LQGVLPALPOVVC 57

RESULT 25
US-08-298-189B-1
; Sequence 1, Application US/08298189B
; Patent No. 5674727
; GENERAL INFORMATION:
; APPLICANT: Dr. Laurence A. Cole and Dr. Andrew Kardana
; TITLE OF INVENTION: No. 5674727el Methods for Detecting Reproductive
; TITLE OF INVENTION: Cancers or Tumors and Assay Products
; TITLE OF INVENTION: Therefor
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Laurence A. Cole , c/o Dept. of Obstetrics and
; STREET: 333 Cedar Street
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06510
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Microsoft Word 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/298,189B
; FILING DATE: 08/31/94
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Brian D. Voyce
; REGISTRATION NUMBER: 28,917
; REFERENCE/DOCKET NUMBER: DS11
; TELEPHONE: 919-638-3939 or 803-272-1471
; TELEFAX: 919-638-3939 or 803-272-1471
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 145 amino acids
; TYPE: amino acid
; STRANDEDNESS: No. 5674727 applicable
; TOPOLOGY: Unknown
; MOLECULE TYPE: subunit of hormone, specifically the
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MOLECULE TYPE: beta\subunit of hCG
ORIGINAL SOURCE: human urine
FEATURE:
NAME/KEY: beta subunit of hCG that is nicked by GBNE
LOCATION: hCG
IDENTIFICATION METHOD: N-terminal sequence analysis
PUBLICATION INFORMATION:
AUTHORS: Keutmann et alia
TITLE: "A Receptor-binding Region in Human
JOURNAL: Proc Nat'l Acad Sci USA
VOLUME: 84
ISSUE: No. 5674727 applicable
PAGES: 2038-2042
DATE: 1987
US-08-298-189B-1

Choriogonadotrophin/Lutoprin H

Query Match 100.0%; Score 67; DB 1; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00046;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LQGVLPALPQVVC 13
Db 45 LQGVLPALPQVVC 57

Search completed: December 4, 2002, 11:29:14
Job time : 11.05 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:27:25 ; Search time 6.5 Seconds
(without alignments)
32.485 Million cell updates/sec

Title: US-09-821-380-2

Perfect score: 67

Sequence: 1 LOGVLPALPQVVC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : Published_Applications_AA:*

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	100.0	13	10	US-09-821-380-2
2	67	100.0	17	10	US-09-821-380-1
3	67	100.0	20	9	US-09-915-676-9
4	67	100.0	20	10	US-09-466-320-6
5	67	100.0	141	9	US-09-813-398-3
6	67	100.0	165	9	US-09-915-676-1
7	67	100.0	165	10	US-09-466-320-14
8	67	100.0	195	10	US-09-780-933-30
9	67	100.0	196	10	US-09-780-933-29
10	67	100.0	307	10	US-09-756-186-4
11	67	100.0	336	10	US-09-756-186-8
12	56	83.6	122	9	US-09-813-398-4
13	52	77.6	10	10	US-09-821-380-3
14	50	74.6	10	10	US-09-821-380-4
15	41	61.2	8	10	US-09-821-380-10
16	41	61.2	113	10	US-09-730-617-44
17	39	58.2	65	10	US-09-764-860-467
18	39	58.2	3594	10	US-09-911-842-4
19	37	55.2	55	10	US-09-864-761-41625

20	37	55.2	99	10	US-09-730-617-41	Sequence 41, Appl
21	37	55.2	141	10	US-09-730-617-47	Sequence 47, Appl
22	37	55.2	141	10	US-09-730-617-48	Sequence 48, Appl
23	37	55.2	654	10	US-09-969-528-10	Sequence 10, Appl
24	36	53.7	7	10	US-09-821-380-11	Sequence 11, Appl
25	36	53.7	114	10	US-09-925-300-1551	Sequence 1551, Ap
26	36	53.7	279	10	US-09-775-879-23	Sequence 23, Appl
27	36	53.7	334	10	US-09-747-835A-32	Sequence 32, Appl
28	35	52.2	7	10	US-09-821-380-9	Sequence 9, Appl
29	35	52.2	115	10	US-09-813-459-25	Sequence 25, Appl
30	35	52.2	119	12	US-10-113-406-16	Sequence 16, Appl
31	35	52.2	120	9	US-09-859-211-42	Sequence 2, Appl
32	35	52.2	120	9	US-09-880-708-20	Sequence 42, Appl
33	35	52.2	120	10	US-09-813-459-16	Sequence 20, Appl
34	35	52.2	125	10	US-09-867-550-658	Sequence 16, Appl
35	35	52.2	214	10	US-09-995-515-5	Sequence 658, App
36	35	52.2	364	9	US-10-060-500-65	Sequence 5, Appl
37	35	52.2	364	12	US-10-117-178-2	Sequence 65, Appl
38	35	52.2	473	9	US-09-813-398-25	Sequence 2, Appl
39	35	52.2	479	9	US-09-813-398-26	Sequence 25, Appl
40	34	50.7	67	10	US-09-864-761-44768	Sequence 26, Appl
41	34	50.7	74	10	US-09-864-761-33496	Sequence 44768, A
42	34	50.7	85	10	US-09-864-761-36293	Sequence 33496, A
43	34	50.7	91	10	US-09-864-761-43325	Sequence 36293, A
44	34	50.7	96	10	US-09-864-761-43325	Sequence 43325, A
45	34	50.7	115	10	US-09-813-459-26	Sequence 454, App
46	34	50.7	120	10	US-09-813-459-6	Sequence 26, Appl
47	34	50.7	131	10	US-09-864-761-46123	Sequence 6, Appl
48	34	50.7	182	10	US-09-764-870-293	Sequence 46123, A
49	34	50.7	226	10	US-09-764-853-593	Sequence 293, App
50	34	50.7	226	10	US-09-764-853-593	Sequence 593, App
51	34	50.7	266	10	US-09-764-898-193	Sequence 266, App
52	34	50.7	275	10	US-09-764-898-193	Sequence 193, App
53	34	50.7	327	10	US-09-790-264-15	Sequence 15, Appl
54	34	50.7	327	10	US-09-925-300-1209	Sequence 1209, Ap
55	34	50.7	350	9	US-09-361-655-14	Sequence 14, Appl
56	34	50.7	414	10	US-09-820-893-69	Sequence 69, Appl
57	34	50.7	457	10	US-09-888-615-110	Sequence 110, App
58	34	50.7	476	10	US-09-813-459-5	Sequence 5, Appl
59	34	50.7	480	10	US-09-820-893-108	Sequence 108, App
60	34	50.7	622	9	US-09-981-353-129	Sequence 129, App
61	34	50.7	643	10	US-09-801-368-236	Sequence 236, App
62	34	50.7	673	10	US-09-782-980-68	Sequence 68, Appl
63	34	50.7	828	8	US-08-681-219-28	Sequence 28, Appl
64	33.5	50.0	3571	10	US-09-911-842-2	Sequence 2, Appl
65	33	49.3	81	10	US-09-815-242-11472	Sequence 11472, A
					US-09-867-550-1944	Sequence 1944, Ap

ALIGNMENTS

RESULT 1

US-09-821-380-2

; Sequence 2, Application US/09821380

; Patent No. US20020064501A1

; GENERAL INFORMATION:

; APPLICANT: Khan, Ahmed

; APPLICANT: Benner, Robbert

; APPLICANT: Savelkoul, Josef

; TITLE OF INVENTION: IMMUNOREGULATOR

; FILE REFERENCE: 2183-479908

; CURRENT APPLICATION NUMBER: US/09/821,380

; PRIOR FILING DATE: 2001-03-29

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: EP 98201695.8

; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: EP 98202706.2

; PRIOR FILING DATE: 1999-08-12

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fragment of peptide immunoregulator
US-09-821-380-2

Query Match          100.0%; Score 67; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
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Db 1 LQGVLPALPQVVC 13

RESULT 2
US-09-821-380-1
; Sequence 1, Application US/09821380
; Patent No. US20020064501A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Ahmed
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-4799US
; CURRENT APPLICATION NUMBER: US/09/821,380
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/NL99/00313
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/???,???
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: EP 98201695.8
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Peptide immunoregulator
US-09-821-380-1

Query Match          100.0%; Score 67; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
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Db 5 LQGVLPALPQVVC 17

RESULT 3
US-09-915-676-9
; Sequence 9, Application US/09915676
; Patent No. US20020164338A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Combined Approach to Treatment of Cancer
; FILE REFERENCE: 50450-8027 US01
; CURRENT APPLICATION NUMBER: US/09/915,676
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 09/571,497
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/134,419
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/134,432
; PRIOR FILING DATE: 1999-05-17

; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-915-676-9

Query Match          100.0%; Score 67; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
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Db 8 LQGVLPALPQVVC 20

RESULT 4
US-09-466-320-6
; Sequence 6, Application US/09466320
; Patent No. US2002025939A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick
; TITLE OF INVENTION: Chorionic Gonadotropin DNA Vaccines and
; FILE REFERENCE: 0450-0026.30
; CURRENT APPLICATION NUMBER: US/09/466,320
; CURRENT FILING DATE: 1999-12-17
; EARLIER APPLICATION NUMBER: US 60/112,910
; EARLIER FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-466-320-6

Query Match          100.0%; Score 67; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
   | | | | | | | | | |
Db 8 LQGVLPALPQVVC 20

RESULT 5
US-09-813-398-3
; Sequence 3, Application US/09813398
; Patent No. US20020169292A1
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
; APPLICANT: Mariusz W. Szkudlinski
; APPLICANT: University of Maryland
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
; FILE REFERENCE: UOFMD.003C1
; CURRENT APPLICATION NUMBER: US/09/813,398
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/05908
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/19772
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 141
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
; OTHER INFORMATION:
US-09-813-398-3
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Query Match 100.0%; Score 67; DB 9; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
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Db 46 LOGVLPALPQVVC 58

RESULT 6
US-09-915-676-1
; Sequence 1, Application US/09915676
; Patent No. US20020164339A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Combined Approach to Treatment of Cancer
; FILE REFERENCE: 50450-8027.US01
; CURRENT APPLICATION NUMBER: US/09/915,676
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 09/571,497
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/134,419
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/134,432
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 165
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; ORGANISM: Homo sapiens
US-09-915-676-1

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Db 65 LOGVLPALPQVVC 77

RESULT 7
US-09-466-320-14
; Sequence 14, Application US/09466320
; Patent No. US20020025939A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick
; TITLE OF INVENTION: Chorionic Gonadotropin DNA Vaccines and
; FILE REFERENCE: 0450-0026.30
; CURRENT APPLICATION NUMBER: US/09/466,320
; CURRENT FILING DATE: 1999-12-17
; EARLIER APPLICATION NUMBER: US 60/112,910
; EARLIER FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hCG beta sub unit
US-09-466-320-14

Query Match 100.0%; Score 67; DB 10; Length 165;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
| | | | | | | | | | | | | | |
Db 65 LOGVLPALPQVVC 77

RESULT 8
US-09-780-933-30
; Sequence 30, Application US/09780933
; Patent No. US20020127652A1
; GENERAL INFORMATION:
; APPLICANT: SCHAMBYE, HANS T.
; APPLICANT: ANDERSEN, KIM V.
; APPLICANT: VAN DEN HAZEL, BART
; APPLICANT: CHRISTIANSEN, JESPER
; APPLICANT: JEPPESEN, CLAUS B.
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
; FILE REFERENCE: 31-001000US
; CURRENT APPLICATION NUMBER: US/09/780,933
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PA 2000 00220
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,035
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PA 2000 01092
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,558
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-933-30

Query Match 100.0%; Score 67; DB 10; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.00031;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
| | | | | | | | | | | | | | |
Db 129 LOGVLPALPQVVC 141

RESULT 9
US-09-780-933-29
; Sequence 29, Application US/09780933
; Patent No. US20020127652A1
; GENERAL INFORMATION:
; APPLICANT: SCHAMBYE, HANS T.
; APPLICANT: ANDERSEN, KIM V.
; APPLICANT: VAN DEN HAZEL, BART
; APPLICANT: CHRISTIANSEN, JESPER
; APPLICANT: JEPPESEN, CLAUS B.
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
; FILE REFERENCE: 31-001000US
; CURRENT APPLICATION NUMBER: US/09/780,933
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PA 2000 00220
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,035
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PA 2000 01092
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,558
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-933-29

Query Match 100.0%; Score 67; DB 10; Length 196;
Best Local Similarity 100.0%; Pred. No. 0.00031;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
| | | | | | | | | |
Db 130 LOGVLPALPQVVC 142

RESULT 10

US-09-756-186-4
; Sequence 4, Application US/09756186
; Patent No. US20010014333A1
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/804,166
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: CAMPBELL-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-756-186-4

Query Match 100.0%; Score 67; DB 10; Length 307;
Best Local Similarity 100.0%; Pred. No. 0.0005;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
| | | | | | | | | |
Db 207 LOGVLPALPQVVC 219

RESULT 11

US-09-756-186-8
; Sequence 8, Application US/09756186
; Patent No. US20010014333A1
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK

STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/804,166
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: CAMPBELL-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-756-186-8

Query Match 100.0%; Score 67; DB 10; Length 336;
Best Local Similarity 100.0%; Pred. No. 0.00055;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
| | | | | | | | | |
Db 236 LOGVLPALPQVVC 248

RESULT 12
US-09-813-398-4
; Sequence 4, Application US/09813398
; Patent No. US20020169292A1
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
; APPLICANT: Mariusz W. Szkudlinski
; APPLICANT: University of Maryland
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
; FILE REFERENCE: UOFMD.003C1
; CURRENT APPLICATION NUMBER: US/09/813,398
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/05908
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/19772
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 122
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
; US-09-813-398-4

Query Match 83.6%; Score 56; DB 9; Length 122;
Best Local Similarity 84.6%; Pred. No. 0.012;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
| | | | | | | | | |
Db 46 LOGVLPALPQVVC 58

RESULT 13
US-09-821-380-3
; Sequence 3, Application US/09821380
; Patent No. US20020064501A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Ahmed
; APPLICANT: Benner, Robbert
; APPLICANT: Savelkoul, Josef
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-4799US
; CURRENT APPLICATION NUMBER: US/09/821,380
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/NL99/00313
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/???,???
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: EP 98201695.8
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fragment of peptide immunoregulator
US-09-821-380-3

Query Match 77.6%; Score 52; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLPALPQVVC 13
Db 1 VLPALPQVVC 10
|||||

RESULT 14
US-09-821-380-4
; Sequence 4, Application US/09821380
; Patent No. US20020064501A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Ahmed
; APPLICANT: Benner, Robbert
; APPLICANT: Savelkoul, Josef
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-4799US
; CURRENT APPLICATION NUMBER: US/09/821,380
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/NL99/00313
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/???,???
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: EP 98201695.8
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fragment of peptide immunoregulator
US-09-821-380-4

Query Match 74.6%; Score 50; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0079;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQGVLPALPQ 10
Db 1 LQGVLPALPQ 10
|||||

RESULT 15
US-09-821-380-10
; Sequence 10, Application US/09821380
; Patent No. US20020064501A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Ahmed
; APPLICANT: Benner, Robbert
; APPLICANT: Savelkoul, Josef
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-4799US
; CURRENT APPLICATION NUMBER: US/09/821,380
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/NL99/00313
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/???,???
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: EP 98201695.8
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fragment of peptide immunoregulator
US-09-821-380-10

Query Match 61.2%; Score 41; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.6e+04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GVLPALPQ 10
Db 1 GVLPALPQ 8
|||||

RESULT 16
US-09-730-617-44
; Sequence 44, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shinkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: No. US20020068279A1e1 Proteins and Nucleic Acids Encoding the
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730,617
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 44
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-730-617-44

Query Match 61.2%; Score 41; DB 10; Length 113;
Best Local Similarity 53.8%; Pred. No. 3.2;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
; : ||||| ||
Db 59 MPAALPAIPQVVC 71

RESULT 17

US-09-764-860-467
; Sequence 467, Application US/09764860
; Patent No. US20020094953A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC008
; CURRENT APPLICATION NUMBER: US/09/764,860
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1198
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-860-467

Query Match 58.2%; Score 39; DB 10; Length 65;
Best Local Similarity 77.8%; Pred. No. 3.8;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LOGVLPALP 9
; : |||||
Db 27 LSGILPALP 35

RESULT 18

US-09-911-842-4
; Sequence 4, Application US/09911842
; Patent No. US20020151483A1
; GENERAL INFORMATION:
; APPLICANT: Weiher, Andrew A.
; APPLICANT: Elliott, Gary S.
; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37592
; CURRENT APPLICATION NUMBER: US/09/911,842
; CURRENT FILING DATE: 2001-07-24
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 3594
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1757)..()
; OTHER INFORMATION: Xaa = any or unknown amino acid
US-09-911-842-4

Query Match 58.2%; Score 39; DB 10; Length 3594;
Best Local Similarity 61.5%; Pred. No. 2.7e+02;
Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13

Db 1467 LDGVLPPLTHAVTC 1479
; : ||||| ||

RESULT 19

US-09-864-761-41625
; Sequence 41625, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-761-41625

Query Match 61.2%; Score 41; DB 10; Length 113;
Best Local Similarity 53.8%; Pred. No. 3.2;
Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
; : ||||| ||
Db 59 MPAALPAIPQVVC 71

US-09-864-761-41625
; Sequence 41625, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 467
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-864-761-41625

```
Query Match          55.2%; Score 37; DB 10; Length 55;
Best Local Similarity 63.6%; Pred. No. 6.7;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 OGVLPAQV 12
   |||:|:|
Db 38 QGRLPRIPQVL 48

RESULT 20
US-09-730-617-41
; Sequence 41, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shimkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: No. US20020068279A1 Proteins and Nucleic Acids Encoding the Same
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730,617
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-730-617-41

Query Match          55.2%; Score 37; DB 10; Length 99;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 VLPALPQVVC 13
   |||:|:|
Db 48 ILPPMPQVVC 57

RESULT 21
US-09-730-617-47
; Sequence 47, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shimkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: No. US20020068279A1 Proteins and Nucleic Acids Encoding the Same
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730,617
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
```

```
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-730-617-47
```

```
Query Match          55.2%; Score 37; DB 10; Length 141;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 VLPALPQVVC 13
   |||:|:|
Db 68 ILPPMPQVVC 77
```

```
RESULT 22
US-09-730-617-48
; Sequence 48, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shimkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: No. US20020068279A1 Proteins and Nucleic Acids Encoding the Same
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730,617
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Ovis aries
US-09-730-617-48
```

```
Query Match          55.2%; Score 37; DB 10; Length 141;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 VLPALPQVVC 13
   |||:|:|
Db 68 ILPPMPQVVC 77
```

```
RESULT 23
US-09-969-528-10
; Sequence 10, Application US/09969528
; Patent No. US20020150567A1
; GENERAL INFORMATION:
; APPLICANT: Pot, David A.
; APPLICANT: Williams, Lewis T.
; APPLICANT: Jefferson, Anne Bennett
; APPLICANT: Majerus, Philip W.
; TITLE OF INVENTION: No. US20020150567A1 Grb2 Associating Protein and Nucleic Acids Encoding Therefor
```

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/969,528
FILING DATE: 01-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/560,005
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Dow, Karen B.
REGISTRATION NUMBER: 29,684
REFERENCE/DOCKET NUMBER: 2307K-0624000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 654 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Region
LOCATION: 1..654
OTHER INFORMATION: /note= "consensus"
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-969-528-10

Query Match 55.2%; Score 37; DB 10; Length 654;
Best Local Similarity 60.0%; Pred. No. 95;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 VLPALPQVC 13
Db 568 LPLLPVVIC 577

RESULT 24
US-09-821-380-11
; Sequence 11, Application US/09821380
; Patent No. US20020084501A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Ahmed
; APPLICANT: Benner, Robbert
; APPLICANT: Savelkoul, Josef
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-4799US
; CURRENT APPLICATION NUMBER: US/09/821,380
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/NL99/00313
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/777,777
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: EP 98201695.8
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 7

; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fragment of peptide immunoregulator
US-09-821-380-11
Query Match 53.7%; Score 36; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.6e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GVLPALP 9
Db 1 GVLPALP 7
RESULT 25
US-09-925-300-1551
; Sequence 1551, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1551
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1551

Query Match 53.7%; Score 36; DB 10; Length 114;
Best Local Similarity 87.5%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GVLPALPQ 10
Db 84 GVLPELPQ 91

Search completed: December 4, 2002, 11:37:19
Job time : 7.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:26:10 ; Search time 134.875 Seconds
(without alignments)
62.143 Million cell updates/sec

Title: US-09-821-380-2
Perfect score: 67
Sequence: 1 LQGVLPALPQWVC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : Pending Patents_AA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	67	100.0	13	1	PCT-US97-11202A-6
3	67	100.0	13	10	US-08-669-654-6
4	67	100.0	13	11	US-08-709-933-6
5	67	100.0	13	16	US-09-220-415-6
6	67	100.0	13	20	US-09-675-362-6

7	67	100.0	13	20	US-09-675-776-6	Sequence 6, Appli
8	67	100.0	13	20	US-09-677-152-6	Sequence 6, Appli
9	67	100.0	13	22	US-09-821-380-2	Sequence 2, Appli
10	67	100.0	13	24	US-10-050-875-6	Sequence 6, Appli
11	67	100.0	14	1	PCT-US97-11202-12	Sequence 12, Appl
12	67	100.0	14	1	PCT-US97-11202-18	Sequence 18, Appl
13	67	100.0	14	1	PCT-US97-11202A-6	Sequence 26, Appl
14	67	100.0	14	1	PCT-US97-11202A-12	Sequence 12, Appl
15	67	100.0	14	1	PCT-US97-11202A-18	Sequence 18, Appl
16	67	100.0	14	1	PCT-US97-11202A-26	Sequence 26, Appl
17	67	100.0	14	10	US-08-669-654-7	Sequence 7, Appli
18	67	100.0	14	11	US-08-709-933-12	Sequence 12, Appl
19	67	100.0	14	11	US-08-709-933-18	Sequence 18, Appl
20	67	100.0	14	11	US-08-709-933-26	Sequence 26, Appl
21	67	100.0	14	16	US-09-220-415-12	Sequence 12, Appl
22	67	100.0	14	16	US-09-220-415-18	Sequence 18, Appl
23	67	100.0	14	16	US-09-220-415-26	Sequence 26, Appl
24	67	100.0	14	20	US-09-675-362-12	Sequence 12, Appl
25	67	100.0	14	20	US-09-675-362-18	Sequence 18, Appl
26	67	100.0	14	20	US-09-675-362-26	Sequence 26, Appl
27	67	100.0	14	20	US-09-675-776-12	Sequence 12, Appl
28	67	100.0	14	20	US-09-675-776-18	Sequence 18, Appl
29	67	100.0	14	20	US-09-675-776-26	Sequence 26, Appl
30	67	100.0	14	20	US-09-677-152-12	Sequence 12, Appl
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35	67	100.0	14	24	US-10-050-875-26	Sequence 26, Appl
36	67	100.0	17	15	US-09-101-283-8	Sequence 8, Appli
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39	67	100.0	20	1	PCT-US00-27741-5	Sequence 5, Appli
40	67	100.0	20	1	PCT-US00-27741-23	Sequence 23, Appl
41	67	100.0	20	8	US-08-406-916B-25	Sequence 25, Appl
42	67	100.0	20	18	US-09-413-564-3	Sequence 3, Appli
43	67	100.0	20	18	US-09-413-564-5	Sequence 5, Appli
44	67	100.0	20	18	US-09-413-564-23	Sequence 23, Appl
45	67	100.0	20	18	US-09-413-564A-18	Sequence 18, Appl
46	67	100.0	20	18	US-09-413-564A-38	Sequence 38, Appl
47	67	100.0	20	18	US-09-413-564A-40	Sequence 40, Appl
48	67	100.0	20	18	US-09-413-564C-18	Sequence 18, Appl
49	67	100.0	20	18	US-09-413-564C-38	Sequence 38, Appl
50	67	100.0	20	18	US-09-413-564C-40	Sequence 40, Appl
51	67	100.0	20	19	US-09-466-320-6	Sequence 6, Appli
52	67	100.0	20	19	US-09-571-497-9	Sequence 9, Appli
53	67	100.0	20	21	US-09-766-397B-6	Sequence 6, Appli
54	67	100.0	20	23	US-09-915-676-9	Sequence 9, Appli
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57	67	100.0	23	16	US-09-220-415-31	Sequence 31, Appl
58	67	100.0	23	20	US-09-675-362-31	Sequence 31, Appl
59	67	100.0	23	20	US-09-675-776-31	Sequence 31, Appl
60	67	100.0	23	20	US-09-677-152-31	Sequence 31, Appl
61	67	100.0	24	1	PCT-US97-11202-30	Sequence 30, Appl
62	67	100.0	24	1	PCT-US97-11202A-30	Sequence 30, Appl
63	67	100.0	24	16	US-09-220-415-30	Sequence 30, Appl
64	67	100.0	24	19	US-09-587-223A-37	Sequence 37, Appl
65	67	100.0	24	19	US-09-587-223A-95	Sequence 95, Appl

ALIGNMENTS

RESULT 1
PCT-US97-11202-6
; Sequence 6, Application PC/TUS9711202
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF
; TITLE OF INVENTION: HIV INFECTION BY ADMINISTRATION OF

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; TITLE OF INVENTION: DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/11202
; FILING DATE: 24-JUN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/709,948
; FILING DATE: 09-SEP-1996
; APPLICATION NUMBER: USSN 08/669,681
; FILING DATE: 24-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-024
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US97-11202-6

Query Match 100.0%; Score 67; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOGVLPALPQVVC 13
Db 1 LOGVLPALPQVVC 13

RESULT 2
PCT-US97-11202A-6
; Sequence 6, Application PC/TUS9711202A
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF
; TITLE OF INVENTION: HIV INFECTION BY ADMINISTRATION OF
; TITLE OF INVENTION: DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/11202A
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; FILING DATE: 24-JUN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/709,948
; FILING DATE: 09-SEP-1996
; APPLICATION NUMBER: USSN 08/669,681
; FILING DATE: 24-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US97-11202A-6

Query Match 100.0%; Score 67; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LOGVLPALPQVVC 13

RESULT 3
US-08-669-654-6
; Sequence 6, Application US/08669654
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHODS OF PROMOTING HEMATOPOIESIS USING
; TITLE OF INVENTION: DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,654
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-669-654-6
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Query Match 100.0%; Score 67; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 LQGVLPALPQVVC 13

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US-08-709-933-6
; Sequence 6, Application US/08709933
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHODS OF TREATMENT OF WASTING SYNDROME
; TITLE OF INVENTION: BASED ON ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC
; TITLE OF INVENTION: GONADOTROPIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,933
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-709-933-6

Query Match 100.0%; Score 67; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 LQGVLPALPQVVC 13

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US-09-220-415-6
; Sequence 6, Application US/09220415
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: Therapeutic Polypeptides from (-hCG and Derivatives
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property/Technology Law

Query Match 100.0%; Score 67; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
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DB 1 LQGVLPALPQVVC 13

RESULT 6
US-09-675-362-6
; Sequence 6, Application US/09675362
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHOD FOR TREATING CANCER
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property/Technology Law
; STREET: P. O. Box 14329
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/675,362
; FILING DATE: 29-Sep-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/220,415
FILING DATE: 24-DEC-1998
APPLICATION NUMBER: PCT/US97/11210
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11209
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11448
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11202
FILING DATE: 24-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Marianne Fullerer
REGISTRATION NUMBER: 39,983
REFERENCE/DOCKET NUMBER: 4115-116 DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-419-9350
TELEFAX: 919-419-9354
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-675-362-6

Query Match 100.0%; Score 67; DB 20; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
Db 1 LOGVLPALPQVVC 13

RESULT 7
US-09-675-776-6
Sequence 6, Application US/09675776
GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
Bryant, Joseph
Lunardi-Iskandar, Yanto
TITLE OF INVENTION: METHOD FOR PROMOTING HEMATOPOIESTIS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Intellectual Property/Technology Law
STREET: P.O. Box 14329
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/675,776
FILING DATE: 29-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/220,415
FILING DATE: 24-DEC-1998
APPLICATION NUMBER: PCT/US97/11210
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11209
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11448
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11202
FILING DATE: 24-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Marianne Fullerer

REGISTRATION NUMBER: 39,983
REFERENCE/DOCKET NUMBER: 4115-116 DIV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-419-9350
TELEFAX: 919-419-9354
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-675-776-6

Query Match 100.0%; Score 67; DB 20; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
Db 1 LOGVLPALPQVVC 13

RESULT 8
US-09-677-152-6
Sequence 6, Application US/09677152
GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
Bryant, Joseph
Lunardi-Iskandar, Yanto
TITLE OF INVENTION: Therapeutic Fractions of Sources of hCG
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Intellectual Property/Technology Law
STREET: P.O. Box 14329
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/677,152
FILING DATE: 02-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/11210
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11209
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11448
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11202
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: USSN 09/220,415
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Steven J. Hultquist
REGISTRATION NUMBER: 28,021
REFERENCE/DOCKET NUMBER: 4115-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-419-9350
TELEFAX: 919-419-9354
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-09-677-152-6

Query Match 100.0%; Score 67; DB 20; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
| | | | | | | | | | | | | | |
Db 1 LOGVLPALPQVVC 13

RESULT 9

US-09-821-380-2
; Sequence 2, Application US/09821380
; GENERAL INFORMATION:
; APPLICANT: Khan, Ahmed
; APPLICANT: Benner, Robbert
; APPLICANT: Saveikouli, Josef
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-4799US
; CURRENT APPLICATION NUMBER: US/09/821.380
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/NL99/00313
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US-09/???, ???
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: EP 98201695.8
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fragment of peptide immunoregulator
US-09-821-380-2

Query Match 100.0%; Score 67; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
| | | | | | | | | | | | | | |
Db 1 LOGVLPALPQVVC 13

RESULT 10

US-10-050-875-6
; Sequence 6, Application US/10050875
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HIV INFECTION
; BY ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/050,875

; FILING DATE: 18-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,948
; FILING DATE: 09-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REFERENCE/DOCKET NUMBER: 8769-016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-050-875-6

Query Match 100.0%; Score 67; DB 24; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
| | | | | | | | | | | | | | |
Db 1 LOGVLPALPQVVC 13

RESULT 11

PCT-US97-11202-12
; Sequence 12, Application PC/TUS9711202
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF
; HIV INFECTION BY ADMINISTRATION OF
; DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/11202
; FILING DATE: 24-JUN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US97/09,948
; FILING DATE: 09-SEP-1996
; APPLICATION NUMBER: US97/08,681
; FILING DATE: 24-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US97-11202-12

Query Match 100.0%; Score 67; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
DB 2 LQGVLPALPQVVC 14

RESULT 12
PCT-US97-11202-18
; Sequence 18, Application PC/TUS9711202
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF
; TITLE OF INVENTION: HIV INFECTION BY ADMINISTRATION OF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/11202
; FILING DATE: 24-JUN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/709,948
; FILING DATE: 09-SEP-1996
; APPLICATION NUMBER: USSN 08/669,681
; FILING DATE: 24-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US97-11202-18

Query Match 100.0%; Score 67; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
DB 1 LQGVLPALPQVVC 13

RESULT 13

PCT-US97-11202-26
; Sequence 26, Application PC/TUS9711202
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF
; TITLE OF INVENTION: HIV INFECTION BY ADMINISTRATION OF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/11202
; FILING DATE: 24-JUN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/709,948
; FILING DATE: 09-SEP-1996
; APPLICATION NUMBER: USSN 08/669,681
; FILING DATE: 24-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
PCT-US97-11202-26

Query Match 100.0%; Score 67; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
DB 2 LQGVLPALPQVVC 14

RESULT 14
PCT-US97-11202A-12
; Sequence 12, Application PC/TUS9711202A
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF
; TITLE OF INVENTION: HIV INFECTION BY ADMINISTRATION OF
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA

ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/11202A
FILING DATE: 24-JUN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/709,948
FILING DATE: 09-SEP-1996
APPLICATION NUMBER: USSN 08/669,681
FILING DATE: 24-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8769-024
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US97-11202A-12

Query Match 100.0%; Score 67; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQGVLPALPQVVC 13
Db 2 LQGVLPALPQVVC 14

RESULT 15
PCT-US97-11202A-18
Sequence 18, Application PC/TUS9711202A
GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
APPLICANT: Bryant, Joseph
APPLICANT: Lunardi-Iskandar, Yanto
TITLE OF INVENTION: TREATMENT AND PREVENTION OF
TITLE OF INVENTION: HIV INFECTION BY ADMINISTRATION OF
TITLE OF INVENTION: DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/11202A
FILING DATE: 24-JUN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/709,948
FILING DATE: 09-SEP-1996
APPLICATION NUMBER: USSN 08/669,681
FILING DATE: 24-JUN-1996
ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8769-024
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US97-11202A-18

Query Match 100.0%; Score 67; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQGVLPALPQVVC 13
Db 1 LQGVLPALPQVVC 13

RESULT 16
PCT-US97-11202A-26
Sequence 26, Application PC/TUS9711202A
GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
APPLICANT: Bryant, Joseph
APPLICANT: Lunardi-Iskandar, Yanto
TITLE OF INVENTION: TREATMENT AND PREVENTION OF
TITLE OF INVENTION: HIV INFECTION BY ADMINISTRATION OF
TITLE OF INVENTION: DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/11202A
FILING DATE: 24-JUN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/709,948
FILING DATE: 09-SEP-1996
APPLICATION NUMBER: USSN 08/669,681
FILING DATE: 24-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8769-024
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
PCT-US97-11202A-26

Query Match

100.0%; Score 67; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
Db 2 LOGVLPALPQVVC 14

RESULT 17
US-08-669-654-7
; Sequence 7, Application US/08669654
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHODS OF PROMOTING HEMATOPOIESTS USING
; TITLE OF INVENTION: DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,654
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: both
; MOLECULE TYPE: peptide
US-08-669-654-7

Query Match 100.0%; Score 67; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
Db 1 LOGVLPALPQVVC 13

RESULT 18
US-08-709-933-12
; Sequence 12, Application US/08709933
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHODS OF TREATMENT OF WASTING SYNDROME
; TITLE OF INVENTION: BASED ON ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,933
FILING DATE: 09-SEP-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8769-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-709-933-12

Query Match 100.0%; Score 67; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
Db 2 LOGVLPALPQVVC 14

RESULT 19
US-08-709-933-18
; Sequence 18, Application US/08709933
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHODS OF TREATMENT OF WASTING SYNDROME
; TITLE OF INVENTION: BASED ON ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,933
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE


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; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 14 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-709-933-18
Query Match          100.0%; Score 67; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
Db 1 LOGVLPALPQVVC 13

RESULT 20
US-08-709-933-26
; Sequence 26, Application US/08709933
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHODS OF TREATMENT OF WASTING SYNDROME
; TITLE OF INVENTION: BASED ON ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC
; TITLE OF INVENTION: GONADOTROPIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,933
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-019
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 14 amino acids
;   TYPE: amino acid
;   TOPOLOGY: circular
;   MOLECULE TYPE: peptide
US-08-709-933-26
Query Match          100.0%; Score 67; DB 11; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
Db 2 LOGVLPALPQVVC 14

RESULT 21
US-09-220-415-12
; Sequence 12, Application US/09220415
; GENERAL INFORMATION:
```

```
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: Therapeutic Polypeptides from (-hCG and Derivatives
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property/Technology Law
; STREET: P.O. Box 14329
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Patent in
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/11210
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11209
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11448
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11202
; FILING DATE: 24-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Steven J. Hultquist
; REGISTRATION NUMBER: 28,021
; REFERENCE/DOCKET NUMBER: 4115-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-419-9350
; TELEFAX: 919-419-9354
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 14 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-09-220-415-12
Query Match          100.0%; Score 67; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
Db 2 LOGVLPALPQVVC 14

RESULT 22
US-09-220-415-18
; Sequence 18, Application US/09220415
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: Therapeutic Polypeptides from (-hCG and Derivatives
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property/Technology Law
; STREET: P.O. Box 14329
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
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; OPERATING SYSTEM: DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/220,415
; FILING DATE: 24-DEC-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/11210
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11209
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11448
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11202
; FILING DATE: 24-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Steven J. Hultquist
; REGISTRATION NUMBER: 28,021
; REFERENCE/DOCKET NUMBER: 4115-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-419-9350
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-220-415-18

Query Match 100.0%; Score 67; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
| | | | | | | | | | | | | | | |
Db 1 LQGVLPALPQVVC 13

RESULT 23
US-09-220-415-26
; Sequence 26, Application US/09220415
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: Therapeutic Polypeptides from (-hcg and Derivatives
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property/Technology Law
; STREET: P.O. Box 14329
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/220,415
; FILING DATE: 24-DEC-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/11210
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11209
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11448
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11202
; FILING DATE: 24-JUN-1998

; ATTORNEY/AGENT INFORMATION:
; NAME: Steven J. Hultquist
; REGISTRATION NUMBER: 28,021
; REFERENCE/DOCKET NUMBER: 4115-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-419-9350
; TELEFAX: 919-419-9354
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-09-220-415-26

Query Match 100.0%; Score 67; DB 16; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
| | | | | | | | | | | | | | | |
Db 2 LQGVLPALPQVVC 14

RESULT 24
US-09-675-362-12
; Sequence 12, Application US/09675362
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHOD FOR TREATING CANCER
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property/Technology Law
; STREET: P.O. Box 14329
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/675,362
; FILING DATE: 29-Sep-2000
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/220,415
; FILING DATE: 24-DEC-1998
; APPLICATION NUMBER: PCT/US97/11210
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11209
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11448
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11202
; FILING DATE: 24-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Marianne Fulerer
; REGISTRATION NUMBER: 39,983
; REFERENCE/DOCKET NUMBER: 4115-116 DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-419-9350
; TELEFAX: 919-419-9354
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-675-362-12

Query Match 100.0%; Score 67; DB 20; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQGVLPALPQVVC 13
|
Db 2 LQGVLPALPQVVC 14
|

RESULT 25

US-09-675-362-18
; Sequence 18, Application US/09675362
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; Bryant, Joseph
; Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHOD FOR TREATING CANCER
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property/Technology Law
; STREET: P.O. Box 14329
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/675,362
; FILING DATE: 29-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/220,415
; FILING DATE: 24-DEC-1998
; APPLICATION NUMBER: PCT/US97/11210
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11209
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11448
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11202
; FILING DATE: 24-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Marianne Fullerer
; REGISTRATION NUMBER: 39,983
; REFERENCE/DOCKET NUMBER: 4115-116 DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-419-9350
; TELEFAX: 919-419-9354
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-675-362-18

Query Match 100.0%; Score 67; DB 20; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQGVLPALPQVVC 13
|
Db 1 LQGVLPALPQVVC 13
|

Search completed: December 4, 2002, 11:36:17
Job time : 135.875 secs

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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:26:40 ; Search time 9.425 Seconds
(without alignments)
84.494 Million cell updates/sec

Title: US-09-821-380-2

Perfect score: 67

Sequence: 1 LGVLPALPQVVC 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 193982 seqs, 61258239 residues

Total number of hits satisfying chosen parameters: 193982

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : Pending Patents_AA_New:*

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- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
- 7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	100.0	13	6	US-10-029-206A-34
2	67	100.0	15	6	US-10-029-206A-165
3	67	100.0	17	6	US-10-029-206A-44
4	67	100.0	17	6	US-10-029-206A-97
5	67	100.0	163	5	US-09-724-676-63209
6	67	100.0	163	5	US-09-724-676-63209
7	67	100.0	165	6	US-10-187-176-7
8	63	94.0	17	6	US-10-029-206A-99
9	61	91.0	17	6	US-10-029-206A-174
10	58	86.6	15	6	US-10-029-206A-164
11	56	83.6	17	6	US-10-029-206A-133
12	56	83.6	127	6	US-10-187-176-8
13	54	80.6	15	6	US-10-029-206A-166
14	53	79.1	17	6	US-10-029-206A-139
15	52	77.6	10	6	US-10-029-206A-20
16	50	74.6	10	6	US-10-029-206A-49
17	50	74.6	14	6	US-10-029-206A-171
18	45	67.2	9	6	US-10-029-206A-157
19	45	67.2	13	6	US-10-029-206A-155
20	43	64.2	9	6	US-10-029-206A-158
21	41	61.2	8	6	US-10-029-206A-33
22	40	59.7	415	6	US-10-266-829-101
23	39	58.2	263	1	PCT-US02-32727-21707
24	38	56.7	9	6	US-10-029-206A-156
25	38	56.7	14	6	US-10-029-206A-108
26	38	56.7	15	6	US-10-029-206A-161

27	38	56.7	410	6	US-10-092-411A-4135	Sequence 4135, Ap
28	38	56.7	827	5	US-09-724-676-96414	Sequence 96414, A
29	38	56.7	827	5	US-09-724-676-96414	Sequence 96414, A
30	38	56.7	835	5	US-09-724-676-96412	Sequence 96412, A
31	38	56.7	835	5	US-09-724-676-96412	Sequence 96412, A
32	38	56.7	890	5	US-09-724-676-96413	Sequence 96413, A
33	38	56.7	890	5	US-09-724-676-96413	Sequence 96413, A
34	38	56.7	920	5	US-09-724-676-96411	Sequence 96411, A
35	38	56.7	920	5	US-09-724-676-96411	Sequence 96411, A
36	37	55.2	83	5	US-09-724-676-89841	Sequence 89841, A
37	37	55.2	83	5	US-09-724-676-89841	Sequence 89841, A
38	37	55.2	878	5	US-09-724-676-96295	Sequence 96295, A
39	37	55.2	878	5	US-09-724-676-96295	Sequence 96295, A
40	37	55.2	888	5	US-09-724-676-96291	Sequence 96291, A
41	37	55.2	888	5	US-09-724-676-96291	Sequence 96291, A
42	37	55.2	904	5	US-09-724-676-96298	Sequence 96298, A
43	37	55.2	904	5	US-09-724-676-96298	Sequence 96298, A
44	37	55.2	913	5	US-09-724-676-96296	Sequence 96296, A
45	37	55.2	913	5	US-09-724-676-96297	Sequence 96297, A
46	37	55.2	913	5	US-09-724-676A-96296	Sequence 96296, A
47	37	55.2	913	5	US-09-724-676A-96297	Sequence 96297, A
48	37	55.2	914	5	US-09-724-676-96294	Sequence 96294, A
49	37	55.2	914	5	US-09-724-676A-96294	Sequence 96294, A
50	37	55.2	918	5	US-09-724-676-96285	Sequence 96285, A
51	37	55.2	918	5	US-09-724-676A-96285	Sequence 96285, A
52	37	55.2	923	5	US-09-724-676-96292	Sequence 96292, A
53	37	55.2	923	5	US-09-724-676-96293	Sequence 96293, A
54	37	55.2	923	5	US-09-724-676-96292	Sequence 96292, A
55	37	55.2	923	5	US-09-724-676A-96293	Sequence 96293, A
56	37	55.2	928	5	US-09-724-676-96301	Sequence 96301, A
57	37	55.2	928	5	US-09-724-676A-96301	Sequence 96301, A
58	37	55.2	944	5	US-09-724-676-96288	Sequence 96288, A
59	37	55.2	944	5	US-09-724-676A-96288	Sequence 96288, A
60	37	55.2	953	5	US-09-724-676-96286	Sequence 96286, A
61	37	55.2	953	5	US-09-724-676-96287	Sequence 96287, A
62	37	55.2	953	5	US-09-724-676A-96286	Sequence 96286, A
63	37	55.2	954	5	US-09-724-676A-96287	Sequence 96287, A
64	37	55.2	954	5	US-09-724-676-96304	Sequence 96304, A
65	37	55.2	954	5	US-09-724-676A-96304	Sequence 96304, A

ALIGNMENTS

RESULT 1
US-10-029-206A-34
; Sequence 34, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029, 206A
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligopeptide
US-10-029-206A-34

Query Match 100.0%; Score 67; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LGVLPALPQVVC 13
Db 1 LGVLPALPQVVC 13

```
RESULT 2
US-10-029-206A-165
; Sequence 165, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 165
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HLA-DRB1*0101
; OTHER INFORMATION: 15-mers
US-10-029-206A-165

Query Match      100.0%; Score 67; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
| | | | | | | | | | | | | | |
Db 1 LOGVLPALPQVVC 13

RESULT 3
US-10-029-206A-44
; Sequence 44, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
; OTHER INFORMATION: signalling molecule
US-10-029-206A-44

Query Match      100.0%; Score 67; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
| | | | | | | | | | | | | | |
Db 5 LOGVLPALPQVVC 17

RESULT 4
US-10-029-206A-97
; Sequence 97, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
```

```
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: A1188972
; NAME/KEY: MISC_FEATURE
; LOCATION: (2)
; OTHER INFORMATION: The (Xaa( at position 2 indicates an unknown amino acid
US-10-029-206A-97
```

```
Query Match      100.0%; Score 67; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.9e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 LOGVLPALPQVVC 13
| | | | | | | | | | | | | | |
Db 5 LOGVLPALPQVVC 17
```

```
RESULT 5
US-09-724-676-63209
; Sequence 63209, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63209
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-724-676-63209
```

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Query Match      100.0%; Score 67; DB 5; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 LOGVLPALPQVVC 13
| | | | | | | | | | | | | | |
Db 63 LOGVLPALPQVVC 75
```

```
RESULT 6
US-09-724-676A-63209
; Sequence 63209, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63209
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION:
US-09-724-676A-63209
```

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Query Match      100.0%; Score 67; DB 5; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.00037;
```

```
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOGVLPALPQVVC 13
Db 63 LOGVLPALPQVVC 75

RESULT 7
US-10-187-176-7
; Sequence 7, Application US/10187176
; GENERAL INFORMATION:
; APPLICANT: JI, Tae H.
; APPLICANT: JI, Inhae
; TITLE OF INVENTION: Agents and Methods for Modulating Interactions Between
; FILE OF INVENTION: Gonadotropin Hormones and Receptors
; FILE REFERENCE: 028750-221
; CURRENT APPLICATION NUMBER: US/10/187,176
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/301,834
; PRIOR FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CG amino acid sequence
US-10-187-176-7

Query Match 100.0%; Score 67; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 0.00038;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOGVLPALPQVVC 13
Db 65 LOGVLPALPQVVC 77

RESULT 8
US-10-029-206A-99
; Sequence 99, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: A1126906
US-10-029-206A-99

Query Match 94.0%; Score 63; DB 6; Length 17;
Best Local Similarity 84.6%; Pred. No. 0.00018;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOGVLPALPQVVC 13
Db 5 MGVLPALPQVVC 17

RESULT 9
US-10-029-206A-174
; Sequence 174, Application US/10029206A
```

```
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 174
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NMPP-71
US-10-029-206A-174

Query Match 91.0%; Score 61; DB 6; Length 17;
Best Local Similarity 92.3%; Pred. No. 0.0004;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LOGVLPALPQVVC 13
Db 5 LPGLPALPQVVC 17

RESULT 10
US-10-029-206A-164
; Sequence 164, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HLA-DRB1*0101
US-10-029-206A-164

Query Match 86.6%; Score 58; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOGVLPALPQVVC 12
Db 4 LOGVLPALPQVVC 15

RESULT 11
US-10-029-206A-133
; Sequence 133, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
```

; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 133

; LENGTH: 17

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: swissnew/P01229/LSHB HUMAN

US-10-029-206A-133

Query Match 83.6%; Score 56; DB 6; Length 17;

Best Local Similarity 84.6%; Pred. No. 0.0028;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQGVLPALPOVVC 13

|| ||| |||||

Db 5 LQAVLPPLPOVVC 17

RESULT 12

US-10-187-176-8

; Sequence 8, Application US/10187176

; GENERAL INFORMATION:

; APPLICANT: Ji, Tae H.

; APPLICANT: Ji, Inhae

; TITLE OF INVENTION: Agents and Methods for Modulating Interactions Between

; TITLE OF INVENTION: Gonadotropin Hormones and Receptors

; FILE REFERENCE: 028750-221

; CURRENT APPLICATION NUMBER: US/10/187,176

; CURRENT FILING DATE: 2002-07-02

; PRIOR APPLICATION NUMBER: US 60/301,834

; PRIOR FILING DATE: 2001-07-02

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8

; LENGTH: 127

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: CG amino acid sequence

US-10-187-176-8

Query Match 83.6%; Score 56; DB 6; Length 127;

Best Local Similarity 84.6%; Pred. No. 0.021;

Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQGVLPALPOVVC 13

|| ||| |||||

Db 51 LQAVLPPLPOVVC 63

RESULT 13

US-10-029-206A-166

; Sequence 166, Application US/10029206A

; GENERAL INFORMATION:

; APPLICANT: Khan, Nisar A.

; APPLICANT: Benner, Robert

; TITLE OF INVENTION: Oligopeptide treatment of anthrax

; FILE REFERENCE: 2183-5222US

; CURRENT APPLICATION NUMBER: US/10/029,206A

; CURRENT FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 09/821,380

; PRIOR FILING DATE: 2001-03-29

; NUMBER OF SEQ ID NOS: 175

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 166

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: HLA-DRB1*0301

; OTHER INFORMATION: (DR17) 15-mers

US-10-029-206A-166

Query Match

Best Local Similarity 80.6%; Score 54; DB 6; Length 15;

Matches 11; Conservative 0; Mismatches 0; Indels 0;

QY 1 LQGVLPALPOV 11

|||||

Db 5 LQGVLPALPOV 15

RESULT 14

US-10-029-206A-139

; Sequence 139, Application US/10029206A

; GENERAL INFORMATION:

; APPLICANT: Khan, Nisar A.

; APPLICANT: Benner, Robert

; TITLE OF INVENTION: Oligopeptide treatment of anthrax

; FILE REFERENCE: 2183-5222US

; CURRENT APPLICATION NUMBER: US/10/029,206A

; CURRENT FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 09/821,380

; PRIOR FILING DATE: 2001-03-29

; NUMBER OF SEQ ID NOS: 175

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 139

; LENGTH: 17

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:

; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN

US-10-029-206A-139

Query Match

Best Local Similarity 79.1%; Score 53; DB 6; Length 17;

Matches 10; Conservative 1; Mismatches 2; Indels 0;

QY 1 LQGVLPALPOVVC 13

|| ||| :||||

Db 5 LQAVLPPLPOVVC 17

RESULT 15

US-10-029-206A-20

; Sequence 20, Application US/10029206A

; GENERAL INFORMATION:

; APPLICANT: Khan, Nisar A.

; APPLICANT: Benner, Robert

; TITLE OF INVENTION: Oligopeptide treatment of anthrax

; FILE REFERENCE: 2183-5222US

; CURRENT APPLICATION NUMBER: US/10/029,206A

; CURRENT FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: 09/821,380

; PRIOR FILING DATE: 2001-03-29

; NUMBER OF SEQ ID NOS: 175

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: oligopeptide

US-10-029-206A-20

Query Match

Best Local Similarity 77.6%; Score 52; DB 6; Length 10;

Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 4 VLPALPOVVC 13

|||||

Db 1 VLPALPOVVC 10

RESULT 16
US-10-029-206A-49
; Sequence 49, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
; OTHER INFORMATION: signalling molecule
US-10-029-206A-49

Query Match 74.6%; Score 50; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOGVLPALPQ 10
| | | | | | | | | |
Db 1 LOGVLPALPQ 10

RESULT 17
US-10-029-206A-171
; Sequence 171, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 171
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NMPP-70
US-10-029-206A-171

Query Match 74.6%; Score 50; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOGVLPALPQ 10
| | | | | | | | | |
Db 5 LOGVLPALPQ 14

RESULT 18
US-10-029-206A-157
; Sequence 157, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US

; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 157
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HLA molecule
; OTHER INFORMATION: type I (A_0201)
US-10-029-206A-157

Query Match 67.2%; Score 45; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GVLPALPQV 11
| | | | | | | | | |
Db 1 GVLPALPQV 9

RESULT 19
US-10-029-206A-155
; Sequence 155, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 155
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Signalp (CBS)
US-10-029-206A-155

Query Match 67.2%; Score 45; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LOGVLPALP 9
| | | | | | | | | |
Db 5 LOGVLPALP 13

RESULT 20
US-10-029-206A-158
; Sequence 158, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 158
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence

;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HLA molecule
; OTHER INFORMATION: type I (A_0201)
US-10-029-206A-158

Query Match 64.2%; Score 43; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VLPALPQVV 12
| | | | | | | | |
DB 1 VLPALPQVV 9

RESULT 21
US-10-029-206A-33
; Sequence 33, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligopeptide

US-10-029-206A-33

Query Match 61.2%; Score 41; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GVLPALPQ 10
| | | | | | | | |
DB 1 GVLPALPQ 8

RESULT 22
US-10-266-829-101
; Sequence 101, Application US/10266829
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 29 Human secreted proteins
; FILE REFERENCE: P2041P1
; CURRENT APPLICATION NUMBER: US/10/266,829
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: 09/756,168
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: PCT/US00/19735
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: 60/145,220
; PRIOR FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-266-829-101

Query Match 59.7%; Score 40; DB 6; Length 415;
Best Local Similarity 77.8%; Pred. No. 34;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGVLPALPQ 10

DB 89 QGLLPSPQ 97
| | | | | | | | |

RESULT 23
PCT-US02-32727-21707
; Sequence 21707, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 21707
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-21707

Query Match 58.2%; Score 39; DB 1; Length 263;
Best Local Similarity 53.8%; Pred. No. 32;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
| | | | | | | | |
DB 150 LAGVLPATVKIMC 162

RESULT 24
US-10-029-206A-156
; Sequence 156, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 156
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HLA molecule
; OTHER INFORMATION: type I (A_0201)
US-10-029-206A-156

Query Match 56.7%; Score 38; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPAL 8
| | | | | | | | |
DB 2 LQGVLPAL 9

```
RESULT 25
US-10-029-206A-108
; Sequence 108, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mm.129320.2
US-10-029-206A-108

Query Match      56.7%; Score 38; DB 6; Length 14;
Best Local Similarity 46.2%; Pred. No. 2.5;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
   :|l:l||::l
DB 2 VQKVPMLPRLLC 14
```

```
Search completed: December 4, 2002, 11:36:51
Job time : 9.425 secs
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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:23:55 ; Search time 11.7 Seconds
(without alignments)
106.816 Million cell updates/sec

Title: US-09-821-380-2
Perfect score: 67
Sequence: 1 LQGVLPALPQVVC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	100.0	145	2	137231
2	67	100.0	165	1	KTHUB
3	56	83.6	141	1	UTRHB
4	53	79.1	165	1	KTBAB
5	43	64.2	304	2	T02911
6	42	62.7	447	2	AE0094
7	41	61.2	102	2	T23320
8	41	61.2	169	1	KTHOB
9	41	61.2	314	2	T16052
10	41	61.2	454	2	C82682
11	40	59.7	817	2	T16409
12	40	59.7	1076	2	C86620
13	39	58.2	89	2	A84086
14	39	58.2	287	2	D96575
15	39	58.2	432	2	C95275
16	39	58.2	1606	2	T49219
17	38	56.7	154	2	C69262
18	38	56.7	266	2	AG0726
19	38	56.7	274	2	F90351
20	38	56.7	338	2	H98233
21	38	56.7	338	2	AD3052
22	38	56.7	447	2	S56546
23	38	56.7	447	2	H91288
24	38	56.7	447	2	C86130
25	38	56.7	459	2	A99932
26	38	56.7	463	2	H70504
27	38	56.7	493	1	F2WLDP
28	38	56.7	532	2	S74453
29	38	56.7	570	2	F87446

30	38	56.7	915	2	T12526
31	38	56.7	998	2	T23427
32	38	56.7	1096	2	H86237
33	38	56.7	1336	2	T39978
34	37	55.2	80	2	I65235
35	37	55.2	119	2	A61465
36	37	55.2	138	2	S00512
37	37	55.2	139	2	I52320
38	37	55.2	141	1	UTRHB
39	37	55.2	141	1	UTBOB
40	37	55.2	141	1	UTSHB
41	37	55.2	141	1	UTPGB
42	37	55.2	141	2	JC4527
43	37	55.2	335	2	AB2165
44	37	55.2	440	2	F70792
45	37	55.2	452	2	T41108
46	37	55.2	477	1	P2WLEP
47	37	55.2	494	2	H82523
48	37	55.2	538	2	J01195
49	37	55.2	646	2	S55048
50	37	55.2	686	1	S28050
51	37	55.2	711	2	T12525
52	37	55.2	776	2	T19900
53	37	55.2	827	2	D96907
54	37	55.2	969	2	S54594
55	37	55.2	1259	2	AE1055
56	37	55.2	2156	1	RRVUNE
57	36	53.7	60	2	T19454
58	36	53.7	139	2	T10040
59	36	53.7	173	2	A11885
60	36	53.7	298	2	S55497
61	36	53.7	301	2	AB3216
62	36	53.7	331	2	AE0093
63	36	53.7	332	2	H90209
64	36	53.7	351	2	T19284
65	36	53.7	400	2	A97535

ALIGNMENTS

RESULT 1
I37231
beta-gonadotropin - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jul-2000
C:Accession: I37231
R:Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
A:Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin Nature 307, 37-40, 1984
A:Reference number: I37231; MUID:84093590; PMID:6690982
A:Accession: I37231
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-145 <RES>
A:Cross-references: EMBL:X00266; NID:g29907; PIDN:CAA25069.1; PID:g1335012
C:Genetics:
A:Introns: 41/3
C:Superfamily: pituitary glycoprotein hormone beta chain
Query Match 100.0%; Score 67; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
Db 45 LQGVLPALPQVVC 57
|||||

RESULT 2
KTHUB
Choriongonadotropin beta chain precursor [validated] - human
N;Alternate names: beta-gonadotropin; chorionic gonadotropin beta chain

C:Species: Homo sapiens (man)
C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 08-Dec-2000
C:Accession: A93230; I55224; I55224; I55224; I70007; I70008; A92303; A92181; A92142; PC1
R:Fiddes, J.C.; Goodman, H.M.
A:Title: The cDNA for the beta-subunit of human chorionic gonadotropin suggests evolution
Nature 286, 684-687, 1980
A:Reference number: A93230; MUID:81012134; PMID:6774259
A:Accession: A93230
A:Molecule type: mRNA
A:Residues: 1-165 <FID>
A:Cross-references: GB:J00117; GB:M38559; GB:M54963; NID:g180436; PIDN:AAA95690.1; PID:9
R:Pollicastro, P.; O'Witt, C.E.; Hoshina, M.; Fukuoaka, H.; Boothby, M.R.; Boime, I.
J. Biol. Chem. 258, 11492-11499, 1983
A:Title: The beta subunit of human chorionic gonadotropin is encoded by multiple genes.
A:Reference number: I55224; MUID:84008141; PMID:6194155
A:Accession: I69972
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-165 <POL>
A:Cross-references: GB:K03189; NID:g180450; PIDN:AAA53288.1; PID:g180453
A:Note: clone CG-beta-e
A:Accession: I55224
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-23, 'M', 25-136, 'A', 138-165 <PO2>
A:Cross-references: GB:K03183; NID:g180442; PIDN:AAA53287.1; PID:g180444
A:Note: clone CG-beta-a
R:Pollicastro, P.F.; Daniels-McQueen, S.; Carle, G.; Boime, I.
J. Biol. Chem. 261, 5907-5916, 1986
A:Title: A map of the hCG beta-LH beta gene cluster.
A:Reference number: I55250; MUID:86195987; PMID:2422163
A:Accession: I55250
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <FO3>
A:Cross-references: GB:M13504; NID:g180419; PIDN:AAA52005.1; PID:g463088
A:Note: CG-beta-3 gene
A:Accession: I70007
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <FO4>
A:Cross-references: GB:M13505; NID:g180429; PIDN:AAA52008.1; PID:g463089
A:Note: CG-beta-6 gene
A:Accession: I70008
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RE5>
A:Cross-references: GB:M13503; NID:g180432; PIDN:AAA52009.1; PID:g463090
A:Note: CG-beta-7 gene
R:Birken, S.; Fetherston, J.; Canfield, R.; Boime, I.
J. Biol. Chem. 256, 1816-1823, 1981
A:Title: The amino acid sequences of the prepeptides contained in the alpha and beta sub
A:Reference number: A92303; MUID:81117268; PMID:7462224
A:Accession: A92303
A:Molecule type: protein
A:Residues: 1-20 <BIR>
A:Note: The identity of the residue at position 19 could not be determined
R:Morgan, F.J.; Birken, S.; Canfield, R.E.
J. Biol. Chem. 250, 5247-5258, 1975
A:Title: The amino acid sequence of human chorionic gonadotropin. The alpha subunit and
A:Reference number: A92181; MUID:75211304; PMID:I150658
A:Accession: A92181
A:Molecule type: protein
A:Residues: 21-165 <MOR>
R:Carlsson, R.B.; Bahl, O.P.; Swaminathan, N.
J. Biol. Chem. 248, 6810-6827, 1973
A:Reference number: A92142; MUID:74011267; PMID:4795659
A:Accession: A92142
A:Molecule type: protein
A:Residues: 21-22, 'Q', 24-73, 'ZL', 76-140, 142-157, 'PB', 160-165, 'SLP' <CAR>
R:Shi, Z.P.; Du, G.G.; Li, W.X.; Liu, X.J.; Li, S.Z.; Xu, Y.S.; Wang, Y.
Chinese Biochem. J. 6, 538-562, 1990
A:Title: The immunological characteristics of the enzymatic fragments of human chorionic

A:Reference number: PC1016
A:Accession: PC1016
A:Molecule type: protein
A:Residues: 21-165 <SHI>
A:Note: article in Chinese with English abstract
R:Birken, S.; Armstrong, E.G.; Kolks, M.A.G.; Cole, L.A.; Agosto, G.M.; Krichesky, A
Endocrinology 123, 572-583, 1988
A:Title: Structure of the human chorionic gonadotropin beta-subunit fragment from pre
A:Reference number: A61097; MUID:88254680; PMID:2454811
A:Accession: A61097
A:Molecule type: protein
A:Residues: 26-32, 'X', 34-49, 'X', 51-60, 75-112 <BI2>
A:Note: this material from pregnancy urine lacks sialic acid in its carbohydrate and h
R:Kardana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.
Br. J. Cancer 67, 686-692, 1993
A:Title: Characterisation of UGP and its relationship with beta-core fragment.
A:Reference number: A56873; MUID:93229246; PMID:8471426
A:Accession: B56873
A:Molecule type: protein
A:Residues: 26-28, 'X', 30-32, 'X', 34-42, 'X', 44-45, 'X', 47-48, 75-76, 'X', 78-91, 'G', 93-102
A:Experimental source: urine
A:Note: sequence modified after extraction from NCBI backbone
A:Note: this material was designated urinary gonadotropin peptide (peak 2)
R:Lapchorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader, J.W.; Canfield, R.E.; Mach
Nature 369, 455-461, 1994
A:Title: Crystal structure of human chorionic gonadotropin.
A:Reference number: A44674; MUID:94261179; PMID:8202136
A:Contents: annotation: X-ray crystallography, 3.0 angstroms; correction of disulfide
R:Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
Nature 307, 37-40, 1984
A:Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin
A:Reference number: I37231; MUID:84093590; PMID:6690982
A:Accession: I37412
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 21-165 <RES>
A:Cross-references: EMBL:X00265; NID:g31719; PIDN:CAA25068.1; PID:g1335075
C:Genetics:
A:Gene: GDB:CGB
A:Cross-references: GDB:I19055; OMIM:118860
A:Map position: 19q13.3-19q13.3
A:Introns: 5/3; 61/3
A:Note: the choriongonadotropin beta chain locus contains six genes (or pseudogenes)
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; hormone; pituitary
F:1-20/Domain: signal sequence #status experimental <SIC>
F:21-165/Product: choriongonadotropin beta chain #status experimental <MAT>
F:29-77/43-92, 46-130, 54-108, 58-110, 113-120/Disulfide bonds: #status experimental
F:33, 50/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:138, 150/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:141, 147, 152, 158/Binding site: carbohydrate (Ser) (covalent) #status experimental
Query Match 100.0%; Score 67; DB 1; Length 165;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LQGVLPALPQVVC 13
Db 65 LQGVLPALPQVVC 77
|||||
RESULT 3
UTRUB
lutropin beta chain precursor [validated] - human
N:Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing
C:Species: Homo sapiens (man)
C:Date: 13-Jul-1981 #sequence_revision 24-Nov-1999 #text_change 20-Apr-2001
C:Accession: I37994; I58013; A90604; A92759; A94466; A01497; B94552
R:Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
Nature 307, 37-40, 1984
A:Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin
A:Reference number: I37231; MUID:84093590; PMID:6690982
A:Accession: I37994

A:Status: preliminary; translated from GB/EMBL/DBJ; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-141 <TAL>
A:Cross-references: GB:X00264; NID:g34351; PIDN:CAA25067.1; PID:g2292893
R:Weiss, J.; Axelrod, L.; Whitcomb, R.W.; Harris, P.E.; Crowley, W.F.; Jameson, J.L.
N. Engl. J. Med. 326, 179-183, 1992
A:Title: Hypogonadism caused by a single amino acid substitution in the beta subunit of
A:Reference number: I58013; MUID:92085985; PMID:1727547
A:Accession: I58013
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 72-73, 'R', 75-76 <WET>
A:Cross-references: GB:S71273; NID:g240572; PIDN:AA014960.1; PID:g4262812
A:Note: mutant sequence from patient with hypogonadism
R:Salram, M.R.; Li, C.H.
Biochim. Biophys. Acta 412, 70-81, 1975
A:Title: Human pituitary lutropin. Isolation, properties, and the complete amino acid sequence
A:Reference number: A90604; MUID:76062547; PMID:1191677
A:Accession: A90604
A:Molecule type: protein
A:Residues: 21-38, 'Q', 40-75, 77-131, 133-134, 'H', 136-137 <SAT>
R:Shome, B.; Parlow, A.F.
J. Clin. Endocrinol. Metab. 36, 618-621, 1973
A:Title: The primary structure of the hormone-specific, beta subunit of human pituitary
A:Reference number: A92759; MUID:73090987; PMID:4685398
A:Accession: A92759
A:Molecule type: protein
A:Residues: 21-38, 'Q', 40-75, 77-131, 133-134, 'H', 136-137 <SHO>
R:Closset, J.; Hennen, G.; Lequin, R.M.
FEBS Lett. 29, 97-100, 1973
A:Title: Human luteinizing hormone the amino acid sequence of the beta subunit.
A:Reference number: A91389; MUID:73221227; PMID:4719207
A:Contents: annotation; partial sequence
R:Ward, D.N.
unpublished results, cited by Closset, J., Hennen, G., and Lequin, R.M., FEBS Lett. 29,
A:Reference number: A94466
A:Accession: A94466
A:Molecule type: protein
A:Residues: 21-38, 'Q', 40-46 <WAR>
A:Note: 28-Val, 33-Arg, and 35-Thr were also found
R:Shome, B.; Parlow, A.F.
submitted to the Atlas, April 1975
A:Reference number: A94552
A:Contents: annotation; binding site
C:Genetics:
A:Gene: GDB:LHB
A:Cross-references: GDB:119364; OMIM:152780
A:Map position: 19q13.3-19q13.3
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: blocked amino end; glycoprotein; hormone; pituitary
F:1-20/Domain: signal sequence #status predicted <Sig>
F:21-141/Product: lutropin beta #status experimental <LTB>
F:21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #stat
F:29-54, 43-77, 46-108, 58-130, 92-120, 110-113/disulfide bonds: #status predicted
F:50/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 83.68; Score 56; DB 1; Length 141;
Best Local Similarity 84.68; Pred. No. 0.014;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
II III IIIII
DB 65 LQAVLPPLPQVVC 77

RESULT 4
KTAB
choriogonadotropin beta chain precursor - olive baboon
C:Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 28-May-1999
C:Accession: A25808
R:Crawford, R.J.; Tregear, G.W.; Niall, H.D.
Gene 46, 161-169, 1986

A:Title: The nucleotide sequences of baboon chorionic gonadotropin beta-subunit genes
A:Reference number: A25808; MUID:87106851; PMID:2433190
A:Accession: A25808
A:Molecule type: mRNA
A:Residues: 1-165 <CRA>
A:Cross-references: GB:M14966; NID:g176572; PIDN:AAA35383.1; PID:g176573
C:Comment: There are at least five copies of CG-related genes and at least two of the
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; hormone; placenta; pregnancy maintenance
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-165/Product: chorionadotropin beta chain #status predicted <CGB>
F:29-77, 43-92, 46-130, 54-108, 58-110, 113-120/disulfide bonds: #status predicted
F:33, 50/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:140, 147, 152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 79.18; Score 53; DB 1; Length 165;
Best Local Similarity 76.9%; Pred. No. 0.055;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
II III IIIII
DB 65 LQAVLPVPQVVC 77

RESULT 5
T02911
hypothetical protein T13J8.210 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 04-Mar-2000
C:Accession: T02911
R:Bevan, M.; Pohl, T.; Weizengger, T.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Sch
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z14766
A:Accession: T02911
A:Molecule type: DNA
A:Residues: 1-304 <BEV>
A:Cross-references: EMBL:AL035524
A:Experimental source: cultivar Columbia; BAC clone T13J8
C:Genetics:
A:Map position: 4
A:Introns: 198/3
A:Note: T13J8.210
C:Superfamily: Arabidopsis thaliana hypothetical protein T13J8.210

Query Match 64.2%; Score 43; DB 2; Length 304;
Best Local Similarity 69.2%; Pred. No. 5.9;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
II III III II
DB 286 LFGVLPPLPLVLC 298

RESULT 6
AE0094
probable gluconate transporter gntP [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AE0094
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AE0094
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-447 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC89616.1; PID:g15978845; GSPDB:GN00175
C:Genetics:
A:Gene: gntP
C:Superfamily: D-serine permease

Query Match 62.7%; Score 42; DB 2; Length 447;
 Best Local Similarity 53.8%; Pred. No. 13;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13

Db 179 IYGVNVAIPSVIC 191

RESULT 7

T23320

hypothetical protein K04G11.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T23320; T26015

R:Baynes, C.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z19726

A:Accession: T23320

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-102 <WIL>

A:Cross-references: EMBL:Z78544; PIDN:CAB01763.1; GSPDB:GN000028; CESP:K04G11.6

A:Experimental source: clone K04G11

R:Smyle, R.

submitted to the EMBL Data Library, August 1998

A:Reference number: Z20132

A:Accession: T26015

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-102 <WIL>

A:Cross-references: EMBL:AL031265; PIDN:CAA20328.1; GSPDB:GN000028; CESP:K04G11.6

A:Experimental source: clone VK04G11

C:Genetics:

A:Gene: CESP:K04G11.6

A:Map position: X

A:Introns: 43/2

C:Superfamily: Caenorhabditis elegans hypothetical protein K04G11.6

Query Match 61.2%; Score 41; DB 2; Length 102;
 Best Local Similarity 63.6%; Pred. No. 4.5;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 GVLPLPQVVC 13

Db 71 GILPLPQVVC 81

RESULT 8

KTHOB

choriogonadotropin beta chain precursor - horse

N:Alternate names: chorionic gonadotropin beta chain (CG); luteinizing hormone (LH) beta

C:Species: Equus caballus (domestic horse)

C:Date: 14-Nov-1983 #sequence_revision 03-May-1996 #text_change 18-Jun-1999

C:Accession: A41917; A29304; A29305; A01503

R:Sherman, G.B.; Wolfe, M.W.; Farmerie, T.A.; Clay, C.M.; Threadgill, D.S.; Sharp, D.C.

Mol. Endocrinol. 6, 951-959, 1992

A:Title: A single gene encodes the beta-subunits of equine luteinizing hormone and chorionic gonadotropin

A:Reference number: A41917; MUID:92357035; PMID:1379674

A:Accession: A41917

A:Molecule type: DNA

A:Residues: 1-169 <SHE>

A:Cross-references: GB:S41704; NID:g252740; PIDN:AAB22775.1; PID:g252741

A:Experimental source: sperm

A:Note: sequence extracted from NCBI backbone (NCBIN:110184, NCBI:110185)

R:Sugino, H.; Bousfield, G.R.; Moore Jr., W.T.; Ward, D.N.

J. Biol. Chem. 262, 8603-8609, 1987

A:Title: Structural studies on equine glycoprotein hormones. Amino acid sequence of equine

A:Reference number: A29304; MUID:87250475; PMID:3298238

A:Accession: A29304

A:Molecule type: protein

A:Residues: 21-169 <SUG>

R:Bousfield, G.R.; Liu, W.K.; Sugino, H.; Ward, D.N.

J. Biol. Chem. 262, 8610-8620, 1987

A:Title: Structural studies on equine glycoprotein hormones. Amino acid sequence of e

A:Reference number: A29305; MUID:87250476; PMID:3298239

A:Accession: A29305

A:Molecule type: protein

A:Residues: 21-169 <BOU>

R:Ward, D.N.; Moore Jr., W.T.; Burleigh, B.D.

J. Protein Chem. 1, 263-280, 1982

A:Title: Structural studies on equine chorionic gonadotropin.

A:Reference number: A01503

A:Accession: A01503

A:Molecule type: protein

A:Residues: 21-40,'Q',42-43,'SK',46,'XXX',51,'T',53-64,'T',66-96,'B',98,'R',100-102,

R:Matsumi, T.; Mizuuchi, T.; Titani, K.; Okinaga, T.; Hoshi, M.; Bousfield, G.R.; Sugi

Biochemistry 33, 14039-14048, 1994

A:Title: Structural analysis of N-linked oligosaccharides of equine chorionic gonadot

A:Reference number: A5952; MUID:95034847; PMID:7524670

A:Contents: annotation; glycosylation

A:Note: horse lutropin and choriongonadotropin beta chains have identical protein chain

C:Superfamily: pituitary glycoprotein hormone; pituitary

C:Keywords: glycoprotein; hormone; pituitary

F:1-20/domain: signal sequence #status predicted <SIG>

F:21-169/product: choriongonadotropin beta chain #status experimental <MAT>

F:29-77,43-92,46-130,54-108,58-110,113-120/disulfide bonds: #status predicted

F:33/binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 61.2%; Score 41; DB 1; Length 169;

Best Local Similarity 53.8%; Pred. No. 7.5;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13

Db 65 MPALPAIPQVVC 77

RESULT 9

T16052

hypothetical protein F13B9.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000

C:Accession: T16052

R:Stellies, L.

submitted to the EMBL Data Library, November 1995

A:Description: The sequence of C. elegans cosmid F13B9.

A:Reference number: Z18453

A:Accession: T16052

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-314 <STE>

A:Cross-references: EMBL:U39853; NID:g1055075; PID:g1055079; PIDN:AAB52629.1; GSPDB:G

A:Experimental source: strain Bristol N2; clone F13B9

C:Genetics:

A:Gene: CESP:F13B9.4

A:Map position: X

A:Introns: 4/3; 71/3; 175/2; 221/2; 264/3

C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom

Query Match 61.2%; Score 41; DB 2; Length 314;

Best Local Similarity 58.3%; Pred. No. 14;

Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 QGVLPALPQVVC 13

Db 248 QGIRPVLNVKC 259

RESULT 10

C82682

glutamate-cysteine ligase precursor XF1428 [imported] - Xylella fastidiosa (strain 9a

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: C82682

R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; MUID:20365717; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: C82682
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-454 <SIM>
 A:Cross-references: GB:AE003973; GB:AE003849; NID:g9106438; PIDN:AAF84237.1; GSPDB:GN001
 A:Experimental source: strain 9a5c
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
 Rodrigues, V.; Rosa, A.J. de M.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 A:Authors: da Silva, A.C.R.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 M.; Teuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF1428

Query Match 61.2%; Score 41; DB 2; Length 454;
 Best Local Similarity 75.0%; Pred. No. 20;
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQGVLPALPQV 12
 ||| |||||
 Db 284 LQGLPALPGVL 295

RESULT 11
 T16409
 hypothetical protein F48E8.6 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T16409
 R:Kirsten, J.
 submitted to the EMBL Data Library, March 1995
 A:Description: The sequence of C. elegans cosmid F48E8.
 A:Reference number: S59413
 A:Accession: T16409
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-817 <KIR>
 A:Cross-references: EMBL:U23514; NID:g746484; PID:g746490; PIDN:AAC46543.1; CESP:F48E8.6
 A:Experimental source: strain Bristol N2
 C:Genetics:
 A:Gene: CESP:F48E8.6
 A:Introns: 107/3; 510/3; 670/3; 733/3

Query Match 59.7%; Score 40; DB 2; Length 817;
 Best Local Similarity 50.0%; Pred. No. 54;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 QGVLPALPQVVC 13
 | | | | |
 Db 375 QTVPLPRLIC 386

RESULT 12
 C96620
 protein T30E16.23 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cross)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: C96620
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: C96620
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1076 <STO>
 A:Cross-references: GB:AE005173; NID:g8778749; PIDN:AAF79757.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: T30E16.23
 A:Map position: 1

Query Match 59.7%; Score 40; DB 2; Length 1076;
 Best Local Similarity 77.8%; Pred. No. 71;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 QVLPALPQV 11
 | | | | |
 Db 754 GTLPALPQI 762

RESULT 13
 A84086
 hypothetical protein BH3489 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: A84086
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: A84086
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-89 <STO>
 A:Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BA807208.1; GSPDB:G
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH3489

Query Match 58.2%; Score 39; DB 2; Length 89;
 Best Local Similarity 63.6%; Pred. No. 8.9;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QGVLPALPQV 12
 | | | | |
 Db 13 QGVMPQPPQVI 23

RESULT 14
 D96575
 probable chalcone isomerase, 94270-95700 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cross)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: D96575
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712

C:Accession: D96575
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-287 <STO>
 C:Cross-references: GB:AE0051173; NID:g10645350; PIDN:AAG21470.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F22G10.11
 A:Map position: 1

Query Match 58.2%; Score 39; DB 2; Length 287;
 Best Local Similarity 46.2%; Pred. No. 29;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
 :||:|:|:|
 Db 1 MDGILAAVPSAVC 13

RESULT 15

C95275
 probable ABC transporter SMA0203 [imported] - Sinorhizobium meliloti (strain 1021) magap
 C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: C95275
 R: Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
 ; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
 Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
 A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
 A:Reference number: A95262; MUID:21396509; PMID:11481432
 A:Accession: C95275
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-432 <KUR>
 A:Cross-references: GB:AE006469; PIDN:AAK64765.1; PID:g14523172; GSPDB:GN00165
 A:Experimental source: Strain 1021, megaplasmid pSymA
 R: Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 pala, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: SMA0203
 A:Genome: plasmid

Query Match 58.2%; Score 39; DB 2; Length 432;
 Best Local Similarity 60.0%; Pred. No. 43;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GVLPALPQV 12
 :||:|:|:|
 Db 302 GILPSLPDIV 311

RESULT 16

T49219
 translation initiation factor eIF-4 gamma homolog F27H5.30 [similarity] - Arabidopsis th
 N:Alternate names: protein F27H5.30
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 20-Jun-2000
 C:Accession: T49219
 R: Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z35018
 A:Accession: T49219
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1606 <RIE>
 A:Cross-references: EMBL:AL163852; GSPDB:GN00061; ATSP:F27H5.30
 A:Experimental source: cultivar Columbia; BAC clone F27H5

C:Genetics:

A:Gene: ATSP:F27H5.30
 A:Map position: 3
 A:introns: 455/3; 1370/2; 1435/2; 1523/1; 1529/1; 1558/3; 1586/2

Query Match 58.2%; Score 39; DB 2; Length 1606;
 Best Local Similarity 63.6%; Pred. No. 1.6e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QGVLPALPQV 12
 :||:|:|:|
 Db 672 QNLLPAIPQAV 682

RESULT 17

C89262
 hypothetical protein AF0099 - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C:Accession: C69262
 R: Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
 Glodok, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: utterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes,
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
 A:Reference number: A69250; MUID:98049343; PMID:9389475
 A:Accession: C69262
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-154 <KLE>
 A:Cross-references: GB:AE001099; GB:AE000782; NID:g2689422; PIDN:AAB91131.1; PID:g265
 C:Superfamily: hypothetical protein sll10658

Query Match 56.7%; Score 38; DB 2; Length 154;
 Best Local Similarity 77.8%; Pred. No. 23;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 QGVLPALPQ 10
 :||:|:|:|
 Db 44 RGVLPALPR 52

RESULT 18

AG0726
 phosphotransferase enzyme II, C component [imported] - Salmonella enterica subsp. ent
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AG0726
 R: Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church
 th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
 , S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
 A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se
 A:Reference number: AB0502; PMID:11677608
 A:Accession: AG0726
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-266 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD05513.1; PID:g16503017; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY1960
 C:Superfamily: phosphotransferase system mannose-specific enzyme II, factor II-P

Query Match 56.7%; Score 38; DB 2; Length 266;
 Best Local Similarity 58.3%; Pred. No. 40;
 Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQGVLPALPQV 12
 :||:|:|:|

Wed Dec 4 11:39:38 2002

us-09-821-380-2.rpr

Qy 2 QGVLPALPQVV 12
 Db 401 QGLLPYSPQVI 411
 Search completed: December 4, 2002, 11:27:17
 Job time : 13.7 secs

A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-447 <HAY>
 A;Cross-references: GB:BA000007; PIDN:BA038703.1; PID:gl3364758; GSPDB:GN00154
 A;Experimental source: strain O157:H7, substrain RIMD 0509952
 C;Genetics:
 A;Gene: EC5280
 C;Superfamily: D-serine permease

Query Match 56.7%; Score 38; DB 2; Length 447;
 Best Local Similarity 46.2%; Pred. No. 67;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LQGVLPALPQVVC 13
 Db 179 IYGLVTIPSVIC 191

RESULT 24

C86130
 gluconate transport system permease 3 [imported] - Escherichia coli (strain O157:H7, sub
 C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence-revision 16-Feb-2001 #text_change 14-Sep-2001
 C;Accession: C86130
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: C86130
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-447 <STO>
 A;Cross-references: GB:AE005174; NID:gl2519331; PIDN:AAG59503.1; GSPDB:GN00145; UWGP:Z59
 A;Experimental source: strain O157:H7, substrain EDL933
 C;Genetics:
 A;Gene: gntP
 C;Superfamily: D-serine permease

Query Match 56.7%; Score 38; DB 2; Length 447;
 Best Local Similarity 46.2%; Pred. No. 67;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LQGVLPALPQVVC 13
 Db 179 IYGLVTIPSVIC 191

RESULT 25

A99932
 hypothetical protein SA2117 [imported] - Staphylococcus aureus (strain N315)
 C;Species: Staphylococcus aureus
 C;Date: 10-May-2001 #sequence-revision 10-May-2001 #text_change 22-Oct-2001
 C;Accession: A99932
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A;Reference number: A89758; MUID:21311952; PMID:11418146
 A;Accession: A99932
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-459 <KUR>
 A;Cross-references: GB:BA000018; PID:gl3702126; PIDN:BA043418.1; GSPDB:GN00149
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: SA2117

Query Match 56.7%; Score 38; DB 2; Length 459;
 Best Local Similarity 63.6%; Pred. No. 69;
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:23:34 ; Search time 6.5 Seconds
(without alignments)
82.953 Million cell updates/sec

Title: US-09-821-380-2
Perfect score: 67
Sequence: 1 LOGVLPALPQVVC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	100.0	165	1 CGHB_HUMAN	P01233 homo sapien
2	56	83.6	141	1 LSHB_HUMAN	P01229 homo sapien
3	53	79.1	165	1 CGHB_PAPAN	P07434 papio anubi
4	47	70.1	164	1 CGHB_CALJA	P51500 callithrix
5	43	64.2	2564	1 SPCO_HUMAN	Q9H254 homo sapien
6	41	61.2	169	1 LSHB_HORSE	P08751 equus caball
7	40	59.7	817	1 YR86_CAEEL	Q09568 caenorhabdi
8	39	58.2	386	1 DCUP_DROVI	O18601 drosophila
9	39	58.2	554	1 GYRA_MYCFV	Q49166 mycobacteri
10	38	56.7	447	1 GNTF_ECOLI	P39373 escherichia
11	38	56.7	463	1 ENGA_MYCTU	O33212 mycobacteri
12	38	56.7	493	1 VL2_PAPVD	P03110 deer papill
13	38	56.7	890	1 IMB2_HUMAN	Q92973 homo sapien
14	38	56.7	1336	1 MAM1_SCHPO	P78966 schizosacch
15	38	56.7	1818	1 Z294_HUMAN	O94822 homo sapien
16	37	55.2	128	1 LSHB_PHOSU	O9QVA9 phodopus su
17	37	55.2	138	1 LSHB_CANFA	P18842 canis famil
18	37	55.2	138	1 LSHB_MACRU	O46483 macropus ru
19	37	55.2	141	1 LSHB_BOVIN	P04651 bos taurus
20	37	55.2	141	1 LSHB_MOUSE	O09108 mus musculu
21	37	55.2	141	1 LSHB_PIG	P01232 sus scrofa
22	37	55.2	141	1 LSHB_RAT	P01231 ovis aries
23	37	55.2	141	1 LSHB_SHEEP	O77805 felis silve
24	37	55.2	143	1 LSHB_FELCA	P11327 european el
25	37	55.2	477	1 VL2_PAPVE	P26209 gallus ps
26	37	55.2	538	1 CH60_BACPD	P55878 gallus gall
27	37	55.2	536	1 GLI_CHICK	P30291 homo sapien
28	37	55.2	646	1 WEE1_HUMAN	P47810 homo sapien
29	37	55.2	646	1 WEE1_MOUSE	O63802 rattus norv
30	37	55.2	646	1 MYBB_CHICK	Q03237 gallus gall
31	37	55.2	686	1 MYBB_MOUSE	P39112 saccharomyc
32	37	55.2	969	1 MSUL_YEAST	P27176 puumala vir
33	37	55.2	2156	1 RPPL_PUUMH	

34	36	53.7	169	1	LSHB_EQUAS	P19794 equus asinu
35	36	53.7	169	1	LSHB_EQUBU	O46641 equus burch
36	36	53.7	298	1	HIS1_CANAL	P46586 candida alb
37	36	53.7	325	1	RCEM_CHRVI	P51763 chromatiu
38	36	53.7	400	1	ISDF_AGR75	Q8UFF4 a ispd/ispf
39	36	53.7	520	1	PHLA_MYCTU	Q04001 mycobacteri
40	36	53.7	523	1	TRPE_HALVO	P33975 halobacteri
41	36	53.7	544	1	CH60_BACHD	O50305 bacillus ha
42	36	53.7	597	1	GLMS_PYRHO	O57981 p glucosami
43	36	53.7	674	1	TML1_ARATH	P33543 arabidopsis
44	36	53.7	701	1	CG1_HUMAN	Q13495 homo sapien
45	36	53.7	801	1	TPR2_HUMAN	Q8UP52 homo sapien
46	35	52.2	80	1	BMP3_BOVIN	P22444 bos taurus
47	35	52.2	105	1	LAC5_MOUSE	P20764 mus musculu
48	35	52.2	118	1	LSHB_BALAC	P33088 balaenopter
49	35	52.2	118	1	LSHB_PHYCA	P25330 physeter ca
50	35	52.2	141	1	LSHB_CERSI	O77835 ceratotheri
51	35	52.2	141	1	LSHB_TRIVU	O46482 trichosurus
52	35	52.2	258	1	SURE_COXBU	Q9K121 coxiella bu
53	35	52.2	268	1	AROK_THEAC	Q9H165 thermoplasm
54	35	52.2	289	1	NK2F_MOUSE	P43688 mus musculu
55	35	52.2	318	1	ONCA_TAETA	P22080 taenia taen
56	35	52.2	364	1	GDF3_HUMAN	O9NR23 homo sapien
57	35	52.2	387	1	SL42_BOVIN	P58875 bos taurus
58	35	52.2	403	1	SL42_HUMAN	Q99MS0 rattus norv
59	35	52.2	403	1	SL42_RAT	P12645 homo sapien
60	35	52.2	472	1	BMP3_HUMAN	P55107 homo sapien
61	35	52.2	478	1	BM3B_HUMAN	O09786 schizosacch
62	35	52.2	535	1	YA98_SCHPO	O9AGE6 listeria mo
63	35	52.2	542	1	CH60_LISMO	P28598 bacillus su
64	35	52.2	543	1	CH60_BACSU	Q9PJ33 chlamydia m
65	35	52.2	610	1	GIDA_CHLMU	

ALIGNMENTS

RESULT 1	CGHB_HUMAN	STANDARD;	PRT;	165 AA.
ID	AC	P01233: Q14000; Q13991;		
DT	21-JUL-1986	(Rel. 01, Created)		
DT	21-JUL-1986	(Rel. 01, Last sequence update)		
DT	16-OCT-2001	(Rel. 40, Last annotation update)		
DE	Chorionadotropin beta chain precursor (Chorionic gonadotropin beta subunit) (CG-beta).			
GN	CGB.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81012134; PubMed=6774259;			
RA	Fiddes J.C., Goodman H.M.;			
RT	"The cDNA for the beta-subunit of human chorionic gonadotropin suggests evolution of a gene by readthrough into the 3'-untranslated region."			
RL	Nature 286:684-687(1980).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84093590; PubMed=6690982;			
RA	Talmadge K., Vamvakopoulos N.C., Fiddes J.C.;			
RT	"Evolution of the genes for the beta subunits of human chorionic gonadotropin and luteinizing hormone."			
RL	Nature 307:37-40(1984).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=84008141; PubMed=6194155;			
RA	Pollicastro P., Ovitt C.E., Hoshina M., Fukuoka H., Boothby M.R., Boime I.;			
RT	"The beta subunit of human chorionic gonadotropin is encoded by multiple genes."			

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J. Biol. Chem. 258:11492-11499(1983).

[4] SEQUENCE OF 1-20. PubMed=7462224;
MEDLINE=81117268; PubMed=7462224;
Birken S., Fetherston J., Canfield R.E., Boime I.;
"The amino acid sequences of the prepeptides contained in the alpha
and beta subunits of human choriongonadotropin.";
J. Biol. Chem. 256:1816-1823(1981).

[5] SEQUENCE OF 21-165.
MEDLINE=75211304; PubMed=1150658;
Morgan F.J., Birken S., Canfield R.E.;
"The amino acid sequence of human chorionic gonadotropin. The alpha
subunit and beta subunit.";
J. Biol. Chem. 250:5247-5258(1975).

[6] PRELIMINARY SEQUENCE OF 21-165.
MEDLINE=74011267; PubMed=4795659;
Carlsen R.B., Bahl O.P., Swaminathan N.;
"Human chorionic gonadotropin. Linear amino acid sequence of the beta
subunit.";
J. Biol. Chem. 248:6810-6827(1973).

[7] SEQUENCE OF 1-5 FROM N.A.
MEDLINE=86195987; PubMed=2422163;
Pollicastro P.F., Daniels-McQueen S., Carle G., Boime I.;
"A map of the hCG beta-LH beta gene cluster.";
J. Biol. Chem. 261:5907-5916(1986).

[8] PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
MEDLINE=81215630; PubMed=7240231;
Mise T., Bahl O.P.;
"Assignment of disulfide bonds in the beta subunit of human chorionic
gonadotropin.";
J. Biol. Chem. 256:6587-6592(1981).

[9] DISULFIDE BONDS.
MEDLINE=90094415; PubMed=1688430;
Saccuzzo Beebe J., Mountjoy K., Krzesicki R.F., Perini F.,
Raddon R.W.;
"Role of disulfide bond formation in the folding of human chorionic
gonadotropin beta subunit into an alpha beta dimer assembly-competent
form.";
J. Biol. Chem. 265:312-317(1990).

[10] STRUCTURE OF CARBOHYDRATES.
MEDLINE=92314469; PubMed=1820200;
Weisshaar G., Hiyama J., Renwick A.G.C.;
"Site-specific N-glycosylation of human chorionic gonadotropin --
structural analysis of glycopeptides by one- and two-dimensional LH
NMR spectroscopy.";
Glycobiology 1:393-404(1991).

[11] X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
MEDLINE=94261179; PubMed=8202136;
Lapthorn A.J., Harris D.C., Littlejohn A., Lustbader J.W.,
Canfield R.E., Machin K.J., Morgan F.J., Isaacs N.W.;
"Crystal structure of human chorionic gonadotropin.";
Nature 369:455-461(1994).

-!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.

-!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.

-!- TISSUE SPECIFICITY: PLACENTA.

-!- DEVELOPMENTAL STAGE: MADE BY THE FIRST TRIMESTER PLACENTA.

-!- PHARMACEUTICAL: Available under the names Novarel (Ferring) and
Profasi (Serono).

-!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
FAMILY.

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DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
 GN beta) (LSH-B) (LH-B).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84093590; PubMed=6690982;
 RA Talmadge K., Vamvakopoulos N.C., Fiddes J.C.;
 RT "Evolution of the genes for the beta subunits of human chorionic
 RT gonadotropin and luteinizing hormone.";
 RL Nature 307:37-40(1984).
 RN [2]
 RP SEQUENCE OF 21-141.
 RX MEDLINE=76062547; PubMed=1191677;
 RA Sairam M.R., Li C.H.;
 RT "Human pituitary lutropin. Isolation, properties, and the complete
 RT amino acid sequence of the beta-subunit.";
 RL Biochim. Biophys. Acta 412:70-81(1975).
 RN [3]
 RP PRELIMINARY SEQUENCE OF 21-141.
 RX MEDLINE=73090987; PubMed=4685398;
 RA Shome B., Farlow A.F.;
 RT "The primary structure of the hormone-specific, beta subunit of human
 RT pituitary luteinizing hormone (hLH).";
 RL J. Clin. Endocrinol. Metab. 36:618-621(1973).
 RN [4]
 RP PRELIMINARY PARTIAL SEQUENCE.
 RX MEDLINE=73221227; PubMed=4719207;
 RA Closset J., Hennen G., Lequin R.M.;
 RT "Human luteinizing hormone. The amino acid sequence of the
 RT subunit.";
 RL FEBS Lett. 29:97-100(1973).
 RN [5]
 RP STRUCTURE OF CARBOHYDRATE.
 RX MEDLINE=91122088; PubMed=1991473;
 RA Weisshaar G., Hiyaama J., Renwick A.G.C., Nimtz M.;
 RT "NMR investigations of the N-linked oligosaccharides at individual
 RT glycosylation sites of human lutropin.";
 RL Eur. J. Biochem. 195:257-268(1991).
 RN [6]
 RP STRUCTURE BY NMR OF 58-77.
 RX MEDLINE=92357029; PubMed=1495492;
 RA Keutmann H.T., Hua Q.-X., Weiss M.A.;
 RT "Structure of a receptor-binding fragment from human luteinizing
 RT hormone beta-subunit determined by [1H]- and [15N]nuclear magnetic
 RT resonance spectroscopy.";
 RL Mol. Endocrinol. 6:904-913(1992).
 RN [7]
 RP VARIANT ARG-74.
 RX MEDLINE=92085985; PubMed=1727547;
 RA Weiss J., Axelrod L., Whitcomb R.W., Harris P.E., Crowley W.F.,
 RA Jameson J.L.;
 RT "Hypogonadism caused by a single amino acid substitution in the beta
 RT subunit of luteinizing hormone.";
 RL New Engl. J. Med. 326:179-183(1992).
 CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
 CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
 CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -!- TISSUE SPECIFICITY: PITUITARY.
 CC -!- DISEASE: DEFECTS IN LH ARE A CAUSE OF HYPOGONADISM WHICH IS
 CC CHARACTERIZED BY INFERTILITY AND PSEUDHERMAPHRODITISM.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
 CC FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X00264; CAA25067.1; -;
 DR EMBL; S71273; AAD14960.1; ALT_SEQ.
 DR PIR; A01497; UTHUB.
 DR HSSP; P01233; 1XUL.
 DR GSPoSuidDB; P01229; -;
 DR Genew; HGNC:6584; LHB.
 DR MIM; 152780; -;
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR002400; GF_Cysknot.
 DR InterPro; IPR001545; Gly_HormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR SMART; SM00068; GHb; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 KW Hormone, Glycoprotein; Signal; Pseudohermaphroditism;
 KW Disease mutation.
 FT SIGNAL 1 20
 FT CHAIN 21 141 LUTROPIN BETA CHAIN.
 FT DISULFID 29 77 BY SIMILARITY.
 FT DISULFID 43 92 BY SIMILARITY.
 FT DISULFID 46 130 BY SIMILARITY.
 FT DISULFID 54 108 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 113 120 BY SIMILARITY.
 FT CARBOHYD 50 50 N-LINKED (GLCNAC...).
 FT VARIANT 74 74 /FTID=CAR_000045.
 FT Q->R (IN HYPOGONADISM; LACK OF
 FT RECEPTOR-BINDING).
 FT /FTID=VAR_003189.
 FT E->Q (IN REF. 2).
 FT MISSING (IN REF. 2).
 FT HPOL -> POH (IN REF. 2).
 SQ SEQUENCE 141 AA; 15345 MW; E411766253113F7C CRC64;
 Query Match 83.6%; Score 56; DB 1; Length 141;
 Best Local Similarity 84.6%; Pred. No. 0.0041;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 1 LQGVLPALPQVVC 13
 |||||
 Db 65 LQAVLPPLPQVVC 77

 RESULT 3
 CGHB_PAPAN
 ID CGHB_PAPAN STANDARD; PRT; 165 AA.
 AC P07434;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Choriogonadotropin beta chain precursor (Chorionic gonadotropin beta
 DE subunit) (CG-beta).
 GN CGB
 OS Papio anubis (Olive baboon).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Papio.
 OX NCBI_TaxID=9555;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87106851; PubMed=2433190;
 RA Crawford R.J., Tregear G.W., Niall H.D.;
 RT "The nucleotide sequences of baboon chorionic gonadotropin
 RT beta-subunit genes have diverged from the human.";
 RL Gene 46:161-169(1986).
 CC -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
 CC ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA

CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
-!- TISSUE SPECIFICITY: PLACENTA.
-!- MISCELLANEOUS: THERE ARE AT LEAST FIVE COPIES OF CG-RELATED GENES
AND AT LEAST TWO OF THESE ARE EXPRESSED IN THE BABOON PLACENTA.
-!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
FAMILY.

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EMBL; M14966; AAA35383.1; -.
DR PIR; A25808; KTBAB.
DR HSP; P01233; 1XUL.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR002400; GF_cysknot.
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
DR Hormone; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 164 CHORIOGONADOTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 151 151 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 164 AA; 17712 MW; 0CD9EDDC3618FA6 CRC64;

Query Match 79.1%; Score 53; DB 1; Length 165;
Best Local Similarity 76.9%; Pred. No. 0.017;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
Db 65 LQAVLPVPQVVC 77
|| ||| :||| ||
|| ||| :||| ||

RESULT 4
CGHB_CALJA STANDARD; PRT; 164 AA.
ID CGHB_CALJA
AC P51500;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Choriogonadotropin beta chain precursor (Chorionic gonadotropin beta
DE subunit) (CG-beta).
GN CGB.
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae;
OC Callithrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96115012; PubMed=7492691;
RA Simula A.P., Amato F., Faast R., Lopata A., Berka J., Norman R.J.;
RT "Luteinizing hormone/chorionic gonadotropin bioactivity in the common

marmoset (Callithrix jacchus) is due to a chorionic gonadotropin
molecule with a structure intermediate between human chorionic
gonadotropin and human luteinizing hormone.";
RL Biol. Reprod. 53:380-389(1995).
CC -!- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- TISSUE SPECIFICITY: PLACENTA.
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
FAMILY.

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EMBL; U04447; AAC00029.1; -.
DR HSP; P01233; 1XUL.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR002400; GF_cysknot.
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
DR Hormone; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 164 CHORIOGONADOTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (BY SIMILARITY).
FT CARBOHYD 151 151 O-LINKED (BY SIMILARITY).
SQ SEQUENCE 164 AA; 17712 MW; 0CD9EDDC3618FA6 CRC64;

Query Match 70.1%; Score 47; DB 1; Length 164;
Best Local Similarity 69.2%; Pred. No. 0.2;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
Db 65 LQVILPPLPQVVC 77
|| ||| :||| ||
|| ||| :||| ||

RESULT 5
SPCO_HUMAN STANDARD; PRT; 2564 AA.
ID SPCO_HUMAN
AC Q9H254; Q9HCD0; Q9H3G8; Q9H1K7; Q9H1K8; Q9H1K9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Spectrin beta chain, brain 3 (Spectrin, non-erythroid beta chain 3)
DE (beta-IV spectrin).
GN SPTB4 OR SPTB3 OR KIAA1642.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21316449; PubMed=11294830;
RA Tse W.T., Tang J., Jin O., Korsgren C., John K.M., Kung A.L.,
RA Gwynn B., Peters L.L., Lux S.E.;

"A new spectrin, beta-IV, has a major truncated isoform that associates with promyelocytic leukemia protein nuclear bodies and the nuclear matrix";
 J. Biol. Chem. 276:23974-23985(2001).

[2]
 SEQUENCE FROM N.A. (ISOFORMS 1 TO 4).
 MEDLINE=20539976; PubMed=11086001;
 Berghs S., Aguijaro D., Dirks R. Jr., Maksimova E., Stabach P.,
 Hermel J.-M., Zhang J.-P., Philbrick W., Slepnev V., Ort F.,
 Solimena M.,
 "BetaIV spectrin, a new spectrin localized at axon initial segments and nodes of ranvier in the central and peripheral nervous system.";
 J. Cell Biol. 151:985-1002(2000).

[3]
 SEQUENCE OF 386-2382 FROM N.A. (ISOFORM 1).

TISSUE=Brain;
 MEDLINE=20450683; PubMed=10997877;

Nayase T., Kikuno R., Nakayama M., Hirotsawa M., Ohara O.;
 "Prediction of the coding sequences of unidentified human genes.

XVIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

DNA Res. 7:273-281(2000).

-1- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2, 3 and 4; are produced by alternative splicing.

-1- TISSUE SPECIFICITY: Abundantly expressed in brain and pancreatic islets.

-1- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.

-1- SIMILARITY: CONTAINS 2 CALPONIN-HOMOLOGY (CH) DOMAINS.

-1- SIMILARITY: CONTAINS 1 PH DOMAIN.

-1- SIMILARITY: CONTAINS 18 SPECTRIN REPEATS.

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 EMBL; AF311855; AAG42473.1; -
 EMBL; AF082075; AAG38874.1; -
 EMBL; AY004226; AAF93171.1; -
 EMBL; AY004226; AAF93172.1; -
 EMBL; AY004227; AAF93173.1; -
 EMBL; AB046862; BAB13468.1; -
 HSP; Q01082; 1BKX.
 Genes; HGNC:14896; SPTBN4.
 MIM; 606214; -
 InterPro; IPR001589; Actbind_actinin.
 InterPro; IPR001715; Calponin-like.
 InterPro; IPR001849; PH.
 InterPro; IPR002017; Spectrin.
 InterPro; IPR001605; Spectrin_PH.
 Pfam; PF00169; PH; 3.
 Pfam; PF00307; CH; 2.
 Pfam; PF00435; spectrin; 56.
 PRINTS; P00683; SPECTRINPH.
 SMART; SM00033; CH; 2.
 SMART; SM00233; PH; 1.
 SMART; SM00150; SPEC; 16.
 PROSITE; PS00019; ACTININ_1; 1.
 PROSITE; PS00020; ACTININ_2; 1.
 PROSITE; PS00021; CH; 2.
 PROSITE; PS00003; PH_DOMAIN; 1.
 Cytoskeleton; Membrane; Repeat; Actin-binding; Capping protein;
 Alternative splicing.
 DOMAIN 1 282
 DOMAIN 61 165 ACTIN-BINDING (BY SIMILARITY).
 DOMAIN 180 282 CH 1.
 REPEAT 309 354 CH 2.
 REPEAT 398 419 SPECTRIN 1.
 REPEAT 429 533 SPECTRIN 2.
 REPEAT 535 642 SPECTRIN 3.
 REPEAT 535 642 SPECTRIN 4.

FT REPEAT 644 771
 FT REPEAT 773 879
 FT REPEAT 881 985
 FT REPEAT 1019 1086
 FT REPEAT 1088 1197
 FT REPEAT 1199 1303
 FT REPEAT 1305 1408
 FT REPEAT 1410 1513
 FT REPEAT 1515 1619
 FT REPEAT 1621 1725
 FT REPEAT 1727 1832
 FT REPEAT 1834 1940
 FT REPEAT 1942 2046
 FT REPEAT 2048 2107
 FT DOMAIN 2118 2527
 FT VARSPLIC 1 1257
 FT VARSPLIC 1258 1286
 FT
 FT VARSPLIC 1287 1309
 FT VARSPLIC 1310 2564
 FT VARSPLIC 2113 2154
 FT
 FT VARSPLIC 2155 2564
 FT CONFLICT 604 608
 FT CONFLICT 714 714
 FT CONFLICT 1189 1189
 FT CONFLICT 1193 1193
 FT CONFLICT 1331 1331
 SQ SEQUENCE 2564 AA; 288982 MW; 52CDE7D1D601ECC CRC64;
 Query Match 64.2%; Score 43; DB 1; Length 2564;
 Best Local Similarity 61.5%; Pred. No. 17;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 LGVLPALPQVVC 13
 ||| | |||
 Db 604 LOGVQPCDPQVIC 616
 RESULT 6
 LSHB_HORSE
 ID LSHB_HORSE STANDARD; PRT; 169 AA.
 AC P08751; P01234;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lutropin/choriogonadotropin beta chain precursor (LSH-B/CG-B) (Luteinizing hormone beta subunit).
 GN LHB.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92357035; PubMed=1379674;
 RA Sherman G.B., Wolfe M.W., Farmerie T.A., Clay C.M., Threadgill D.S., Sharp D.C., Nilson J.H.;
 RA "A single gene encodes the beta-subunits of equine luteinizing hormone and chorionic gonadotropin.";
 RL Mol. Endocrinol. 6:951-959(1992).
 RN [2]
 RP SEQUENCE OF 21-169.
 RX MEDLINE=87250476; PubMed=3298239;
 RA Bousfield G.R., Liu W.-K., Sugino H., Ward D.N.;
 RA "Structural studies on equine glycoprotein hormones. Amino acid sequence of equine lutropin beta-subunit.";
 RL J. Biol. Chem. 262:8610-8620(1987).
 RN [3]
 RP SEQUENCE OF 21-169.
 RX MEDLINE=87250475; PubMed=3298238;

OS Drosophila virilis (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7244;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gao L., Wang S., Hickey D.A.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: Uroporphyrinogen-III - coproporphyrinogen + 4
 CO(2).
 CC -!- PATHWAY: PORPHYRIN AND HEME BIOSYNTHESIS.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE UROPORPHYRINOGEN DECARBOXYLASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: U93213; AAB66372.1;
 DR HSP; P06132; IUR0.
 DR FlyBase: FBgn0020672; Dvir\Upd0.
 DR InterPro: IPR000257; Uro_decabxyls.
 DR Pfam: PF01208; URO-D; 1.
 DR PROSITE: PS00906; UROD_1; 1.
 DR PROSITE: PS00907; UROD_2; 1.
 KW Lyase; Decarboxylase; Porphyrin biosynthesis; Heme biosynthesis.
 SQ SEQUENCE 386 AA; 43023 MW; A19F8CC5F17DF6D CRC64;
 Query Match 58.2%; Score 39; DB 1; Length 386;
 Best Local Similarity 63.6%; Pred. No. 13;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 3 GVLPLPQVC 13
 ||| ||| :
 DB 110 GVGPLPQPC 120
 RESULT 9
 ID GYRA_MYCFV STANDARD; PRT; 554 AA.
 AC Q49166;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA gyrase subunit A (EC 5.99.1.3) [Contains: Mfl gyra intein]
 DE (Fragment).
 GN GYRA.
 OS Mycobacterium flavescens.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1776;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FLA0 / 930991;
 RX MEDLINE=96194983; PubMed=8622949;
 RA Fsihi H., Vincent V., Cole S.T.;
 RT "Homing events in the gyra gene of some mycobacteria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:3410-3415(1996).
 CC -!- FUNCTION: DNA GYRASE NEGATIVELY SUPERCOILS CLOSED CIRCULAR DOUBLE-
 CC STRANDED DNA IN AN ATP-DEPENDENT MANNER AND ALSO CATALYZES THE
 CC INTERCONVERSION OF OTHER TOPOLOGICAL ISOMERS OF DOUBLE-STRANDED
 CC DNA RINGS, INCLUDING CATENANES AND KNOTTED RINGS.
 CC -!- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
 CC of double-stranded DNA.
 CC -!- SUBUNIT: MADE UP OF TWO CHAINS. THE A CHAIN IS RESPONSIBLE FOR DNA
 CC BREAKAGE AND REJOINING; THE B CHAIN CATALYZES ATP HYDROLYSIS. THE
 CC ENZYME FORMS AN A2B2 TETRAMER.
 CC -!- PTM: THIS PROTEIN UNDERGOES A PROTEIN SELF SPLICING THAT INVOLVES

CC A POST-TRANSLATIONAL EXCISION OF THE INTERVENING REGION (INTEIN)
 CC FOLLOWED BY PEPTIDE LIGATION (BY SIMILARITY).
 CC -!- SIMILARITY: IN THE INTEIN SECTION; BELONGS TO THE HOMING
 CC ENDONUCLEASE FAMILY.
 CC -----
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 CC EMBL: Z68209; CAA92433.1;
 DR HSP; P72065; IAM2.
 DR InterPro: IPR002205; DNA_topoisoIV.
 DR InterPro: IPR003586; Hedgehog_hintC.
 DR InterPro: IPR003587; Hedgehog_hintN.
 DR InterPro: IPR002203; Intein.
 DR InterPro: IPR004042; Intein_endonuc.
 DR Pfam: PF00521; DNA_topoisoIV; 2.
 DR ProDom: PD000742; DNA_topoisoIV; 2.
 DR SMART: SM00305; HintC; 1.
 DR SMART: SM00306; HintN; 1.
 DR SMART: SM00434; TOP4C; 1.
 DR PROSITE: PS50818; INTEIN_C_TER; 1.
 DR PROSITE: PS50819; INTEIN_ENDONUCLEASE; 1.
 DR PROSITE: PS50817; INTEIN_N_TER; 1.
 KW Topoisomerase; Isomerase; DNA-binding; Autocatalytic cleavage;
 KW Protein splicing; Hydrolase; Nuclease; Endonuclease; Intronic homing.
 FT NON_TER 1 1
 FT CHAIN <1 69 DNA GYRASE SUBUNIT A, 1ST PART (BY
 FT SIMILARITY).
 FT CHAIN 70 490 MFL GYRA INTEIN (BY SIMILARITY).
 FT CHAIN 491 >554 DNA GYRASE SUBUNIT A, 2ND PART (BY
 FT SIMILARITY).
 FT ACT_SITE 69 69 DNA CLEAVAGE (BY SIMILARITY).
 FT NON_TER 554 554
 FT SEQUENCE 554 AA; 60952 MW; EB8209BBCAAD7765 CRC64;
 Query Match 58.2%; Score 39; DB 1; Length 554;
 Best Local Similarity 80.0%; Pred. No. 19;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LOGVLPLPQ 10
 |||:| |||
 DB 374 LOGLLDALPQ 383
 RESULT 10
 ID GNTF_ECOLI STANDARD; PRT; 447 AA.
 AC P39373;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE High-affinity gluconate transporter (Gluconate permease 3) (Gnt-III
 DE system).
 GN GNTP OR B4321 OR Z5919 OR ECS5280.
 OS Escherichia coli, and
 OS Escherichia coli O157:H7.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562, 83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=96125229; PubMed=8550444;
 RA Klemm P., Tong S., Nielsen H., Conway T.;
 RT "The gntP gene of Escherichia coli involved in gluconate uptake.";
 RL J. Bacteriol. 178:161-67(1996).
 RN [2]
 RP SEQUENCE FROM N.A.

CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
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CC -----
CC EMBL; Y00518; CRA68572.1; -.
CC HIR; S00512; S00512.
CC HSP; P01233; 1XUL.
CC InterPro; IPR000359; Cys_knot.
CC InterPro; IPR001545; Gly_hormoneB.
CC Pfam; PF00007; Cys_knot; 1.
CC SMART; SM00068; GHb; 1.
CC PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
CC PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
CC Hormone; Signal; Glycoprotein.
CC NON_TER 1
CC SIGNAL <1 17 LUTROPIN BETA CHAIN.
CC CHAIN 18 138 BY SIMILARITY.
CC DISULFID 26 74 BY SIMILARITY.
CC DISULFID 40 89 BY SIMILARITY.
CC DISULFID 43 127 BY SIMILARITY.
CC DISULFID 51 105 BY SIMILARITY.
CC DISULFID 55 107 BY SIMILARITY.
CC DISULFID 110 117 BY SIMILARITY.
CC CARBOHYD 30 30 N-LINKED (GLCNAC...) (PROBABLE).
CC SEQUENCE 138 AA; 14594 MW; E3639FE6B03F1948 CRC64;
CC
CC Query Match 55.2%; Score 37; DB 1; Length 138;
CC Best Local Similarity 53.8%; Pred. No. 11;
CC Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
CC
CC QY 1 LQGVLPALPQVVC 13
CC | || :|| |
CC Db 62 LPAALPPVPQVVC 74
CC
CC RESULT 18
CC LSHB_MACRU
CC ID LSHB_MACRU STANDARD; PRT; 138 AA.
CC AC O46483;
CC DT 30-MAY-2000 (Rel. 39, Created)
CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
CC DE beta) (LSH-B) (LH-B) (Fragment).
CC GN LHB.
CC OS Macropus rufus (Red kangaroo) (Megalania rufa).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Theria; Diprotodontia; Macropodidae; Macropus.
CC OX NCBI_TaxID=9321;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC TISSUE=Pituitary;
CC RX MEDLINE=98345424; PubMed=9680384;
CC RA Harrison G.A., Deane E.M., Cooper D.W.;
CC RT "CDNA cloning of luteinizing hormone subunits from brushtail possum
CC and red kangaroo."
CC RL Mamm. Genome 9:638-642(1998).
CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.

CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC -----
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CC -----
CC EMBL; AF017450; AAC96021.1; -.
CC HSP; P01233; 1XUL.
CC InterPro; IPR000359; Cys_knot.
CC InterPro; IPR001545; Gly_hormoneB.
CC Pfam; PF00007; Cys_knot; 1.
CC SMART; SM00068; GHb; 1.
CC PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
CC PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
CC Hormone; Signal; Glycoprotein.
CC NON_TER 1
CC SIGNAL <1 19 POTENTIAL.
CC CHAIN 20 138 LUTROPIN BETA CHAIN.
CC DISULFID 27 75 BY SIMILARITY.
CC DISULFID 41 90 BY SIMILARITY.
CC DISULFID 44 128 BY SIMILARITY.
CC DISULFID 52 106 BY SIMILARITY.
CC DISULFID 56 108 BY SIMILARITY.
CC DISULFID 111 118 BY SIMILARITY.
CC CARBOHYD 31 31 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 138 AA; 14698 MW; 2460213836DBFA7B CRC64;
CC
CC Query Match 55.2%; Score 37; DB 1; Length 138;
CC Best Local Similarity 53.8%; Pred. No. 11;
CC Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
CC
CC QY 1 LQGVLPALPQVVC 13
CC | || :|| |
CC Db 63 LPAALPPSPQVVC 75
CC
CC RESULT 19
CC LSHB_BOVIN
CC ID LSHB_BOVIN STANDARD; PRT; 141 AA.
CC AC P04651;
CC DT 13-AUG-1987 (Rel. 05, Created)
CC DT 01-JAN-1988 (Rel. 06, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
CC DE beta) (LSH-B) (LH-B).
CC GN LHB.
CC OS Bos taurus (Bovine).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Theria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC OC Bovidae; Bovinae; Bos.
CC OX NCBI_TaxID=9913;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=85207729; PubMed=2987241;
CC RA Virgin J.B., Silver B.J., Thomason A.R., Nilson J.H.;
CC RT "The gene for the beta subunit of bovine luteinizing hormone encodes
CC a gonadotropin mRNA with an unusually short 5'-untranslated region."
CC J. Biol. Chem. 260:7072-7077(1985).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=85182575; PubMed=3838746;
CC RA Maurer R.A.;
CC RT "Analysis of several bovine lutropin beta subunit cDNAs reveals
CC heterogeneity in nucleotide sequence."
CC J. Biol. Chem. 260:4684-4687(1985).
CC RN [3]
CC RP SEQUENCE OF 21-139.
CC RX MEDLINE=74075724; PubMed=4770795;

RA Maghain-Reginster G., Hennen G.;
 RT "Luteinizing hormone. The primary structures of the beta-subunit from
 RL Eur. J. Biochem. 39:235-253(1973).
 CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
 CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
 CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL; M10077; AAA30623.1; -;
 CC EMBL; M11506; AAB59267.1; -;
 CC PIR; A01499; UTBOB.
 CC HSP; P01233; IXUL.
 CC GlycoSuiteDB; P04651; -;
 CC InterPro; IPR000359; Cys_knot.
 CC InterPro; IPR002400; GF_cysknot.
 CC InterPro; IPR001545; Gly_hormoneB.
 CC Pfam; PF00007; Cys_knot; 1.
 CC PRINTS; PR00438; GFCYSKNOT.
 CC SMART; SM00068; GHb; 1.
 CC PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 CC PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 CC Hormone; Signal; Glycoprotein.
 CC SIGNAL 1 20
 CC CHAIN 21 141 LUTROPIN BETA CHAIN.
 CC FT DISULFID 29 77 BY SIMILARITY.
 CC FT DISULFID 43 92 BY SIMILARITY.
 CC FT DISULFID 46 130 BY SIMILARITY.
 CC FT DISULFID 54 108 BY SIMILARITY.
 CC FT DISULFID 58 110 BY SIMILARITY.
 CC FT DISULFID 113 120 BY SIMILARITY.
 CC FT CARBOHYD 33 33 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CONFLICT 74 74 MISSING (IN REF. 2).
 CC FT CONFLICT 112 112 Q -> E (IN REF. 3).
 CC FT CONFLICT 122 123 P -> S (IN REF. 2).
 CC FT CONFLICT 126 126 GP -> PG (IN REF. 3).
 CC FT CONFLICT 126 126 Q -> E (IN REF. 3).
 CC SEQUENCE 141 AA; 15202 MW; 44FB1CBD4901BC95 CRC64;
 Query Match 55.2%; Score 37; DB 1; Length 141;
 Best Local Similarity 60.0%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 4 VLPALPQVVC 13
 Db 68 ILPPMPQVVC 77
 RESULT 20
 LSMB_MOUSE
 ID LSMB_MOUSE STANDARD; PRT; 141 AA.
 AC 009108; Q60844;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
 DE beta) (LSH-B) (LH-B).
 GN LHB.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=96125216; PubMed=8543188;
 RA Kumar T.R., Matzuk M.M.;
 RT "Cloning of the mouse gonadotropin beta-subunit-encoding genes, II.
 RT Structure of the luteinizing hormone beta-subunit-encoding genes.";
 RL Gene 166:335-336(1995).
 RN [2]
 RP SEQUENCE OF 18-122 FROM N.A.
 RC STRAIN=C57BL/6 X CBA; TISSUE=Anterior pituitary;
 RA Brown P., Brooks J., McNeilly J.R., McNeilly A.S.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
 CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
 CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
 CC FAMILY.
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 CC -----
 CC EMBL; U25145; AAA92841.1; -;
 CC EMBL; Y10418; CAA71445.1; -;
 CC HSP; P01233; IXUL.
 CC MGD; MGI:96782; Lhb.
 CC InterPro; IPR000359; Cys_knot.
 CC InterPro; IPR001545; Gly_hormoneB.
 CC Pfam; PF00007; Cys_knot; 1.
 CC SMART; SM00068; GHb; 1.
 CC PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 CC PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 CC Hormone; Signal; Glycoprotein.
 CC SIGNAL 1 20
 CC CHAIN 21 141 LUTROPIN BETA CHAIN.
 CC FT DISULFID 29 77 BY SIMILARITY.
 CC FT DISULFID 43 92 BY SIMILARITY.
 CC FT DISULFID 54 108 BY SIMILARITY.
 CC FT DISULFID 58 110 BY SIMILARITY.
 CC FT DISULFID 113 120 BY SIMILARITY.
 CC FT CARBOHYD 33 33 N-LINKED (GLCNAC...) (POTENTIAL).
 CC FT CONFLICT 83 83 A -> R (IN REF. 2).
 CC SEQUENCE 141 AA; 15028 MW; 5E997CABF33D90BF CRC64;
 Query Match 55.2%; Score 37; DB 1; Length 141;
 Best Local Similarity 53.8%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 LQGVLPALPQVVC 13
 Db 65 LPAALPPVQVVC 77
 RESULT 21
 LSMB_PIG
 ID LSMB_PIG STANDARD; PRT; 141 AA.
 AC P01232;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
 DE beta) (LSH-B) (LH-B).
 GN LHB.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
[1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91063934; PubMed=1701088;
R Ezashi T., Hirai T., Kato T., Wakabayashi K., Kato Y.;
RT "The gene for the beta subunit of porcine LH: clusters of GC boxes
FT and CACCC elements.";
RL J. Mol. Endocrinol. 5:137-146(1990).
[2]
RP SEQUENCE FROM N.A.
RA MEDLINE=89306142; PubMed=2744222;
R Kato Y., Hirai T.;
RT "Cloning and DNA sequence analysis of the cDNA for the precursor of
FT porcine luteinizing hormone (LH) beta subunit.";
RL Mol. Cell. Endocrinol. 62:47-53(1989).
[3]
RP SEQUENCE OF 21-139.
R MEDLINE=74075724; PubMed=4770795;
RA Maghain-Register G., Hennen G.;
RT "Luteinizing hormone. The primary structures of the beta-subunit from
FT bovine and porcine species.";
RL Eur. J. Biochem. 39:235-253(1973).
CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC
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CC
DR EMBL; D00579; BAA00457.1; -
DR PIR; A30322; UTPGB.
DR PIR; A48170; A48170.
DR HSSP; P01233; 1XUL.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Signal; Glycoprotein.
FT SIGNAL 1 20 LUTROPIN BETA CHAIN.
FT CHAIN 21 141
FT DISULFID 29 92 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .).
FT MOD_RES 21 21 BLOCKED.
FT VARIANT 30 30 R -> Z.
FT CONFLICT 40 40 N -> D (IN REF. 3).
FT CONFLICT 62 62 V -> R (IN REF. 3).
FT CONFLICT 83 83 S -> I (IN REF. 3).
FT CONFLICT 87 87 I -> S (IN REF. 3).
FT CONFLICT 122 123 GP -> PG (IN REF. 3).
SQ SEQUENCE 141 AA; 14889 MW; 803E8E7C59F3C2CF CRC64;

Query Match 55.2%; Score 37; DB 1; Length 141;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 LOGVLPALPQVVC 13
| | | : | | | |
Db 65 LPAALPPVPQVVC 77
RESULT 22
LSHB_RAT STANDARD; PRT; 141 AA.
ID LSHB_RAT
AC P01230;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B).
GN LHB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=83273673; PubMed=6192440;
RA Chin W.W., Godine J.E., Klein D.R., Chang A.S., Tan L.K.,
RA Habener J.F.;
RT "Nucleotide sequence of the cDNA encoding the precursor of the beta
RT subunit of rat lutropin.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4649-4653(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85080043; PubMed=6096374;
RA Jameson L., Chin W.W., Hollenberg A.N., Chang A.S., Habener J.F.;
RT "The gene encoding the beta-subunit of rat luteinizing hormone."
RT Analysis of gene structure and evolution of nucleotide sequence.";
RL J. Biol. Chem. 259:15474-15480(1984).
RN [3]
RP SEQUENCE OF 4-141 FROM N.A.
RC STRAIN=Wistar Imamichi; TISSUE=Anterior pituitary;
RA Kato Y., Ezashi T., Hirai T., Kato T.;
RT "Strain difference in nucleotide sequences of rat glycoprotein hormone
RT subunit cDNAs and gene fragment.";
RL Zool. Sci. 7:877-885(1990).
CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC
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CC
DR EMBL; V01542; CAA24783.1; -
DR EMBL; J00749; AAA96703.1; -
DR EMBL; D00576; BAA00454.1; -
DR PIR; A01498; UTRTB.
DR PIR; S42527; S42527.
DR HSSP; P01233; 1XUL.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.

```

KW Hormone; Signal; Glycoprotein.
FT SIGNAL 1 20
FT CHAIN 21 141 LUTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC... (PROBABLE).
SQ SEQUENCE 141 AA; 15177 MW; 50796FBBE32F83BF CRC64;

Query Match 55.2%; Score 37; DB 1; Length 141;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
| : : : : :
Db 65 LPAALPVPQVVC 77

RESULT 23
LSHB_SHEEP STANDARD; PRT; 141 AA.
ID LSHB_SHEEP STANDARD; PRT; 141 AA.
AC P01231;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lutropin beta chain precursor (luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B) (Interstitial cell stimulating hormone).
DE LHB.
GN Ovis aries (Sheep).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RN SEQUENCE FROM N.A.
RA MEDLINE=93351742; PubMed=8349025;
RX Brown P., McNeilly J.R., Wallace R.M., McNeilly A.S., Clark A.J.;
RT "Characterization of the ovine LH beta-subunit gene: the promoter
RT directs gonadotrope-specific expression in transgenic mice.";
RL Mol. Cell. Endocrinol. 93:157-165(1993).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RX MEDLINE=90245669; PubMed=2336396;
RA D'Angelo-Bernard G., Mounni M., Jutisz M., Counis R.;
RT "Cloning and sequence analysis of the cDNA for the precursor of the
RT beta subunit of ovine luteinizing hormone.";
RL Nucleic Acids Res. 18:2175-2175(1990).
RN [3]
RN SEQUENCE OF 21-139.
RP MEDLINE=72211145; PubMed=4556309;
RA Liu W.-K., Nahn H.S., Sweeney C.M., Holcomb G.N., Ward D.N.;
RT "The primary structure of ovine luteinizing hormone. II. The amino
RT acid sequence of the reduced, S-carboxymethylated A-subunit (LH-
RT beta).";
RL J. Biol. Chem. 247:4365-4381(1972).
RN [4]
RN SEQUENCE OF 21-139.
RP MEDLINE=73190035; PubMed=4575435;
RA Sairam M.R., Samy T.S.A., Papkoff H., Li C.H.;
RT "The primary structure of ovine interstitial cell-stimulating
RT hormone. II. The beta-subunit.";
RL Arch. Biochem. Biophys. 153:572-586(1972).
RN [5]
RN PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.
RX MEDLINE=76068152; PubMed=1201911;
RA Chung D., Sairam M.R., Li C.H.;
RT "The primary structure of ovine interstitial cell stimulating
RT hormone. IV: Disulfide bridges of the beta subunit.";
RL Int. J. Pept. Protein Res. 7:487-493(1975).

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RN [6]
RP STRUCTURE OF CARBOHYDRATE.
RX MEDLINE=91006170; PubMed=2209620;
RA Weisshaar G., Hiyama J., Renwick A.G.C.;
RT "Site-specific N-glycosylation of ovine lutropin. Structural analysis
RT by one- and two-dimensional 1H-NMR spectroscopy.";
RL Eur. J. Biochem. 192:741-751(1990).
CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC
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CC
CC EMBL; S64695; AAB27819.1; -.
CC EMBL; X52488; CAA36729.1; -.
CC PIR; A01500; UTSBH.
CC PIR; S09232; S09232.
CC HSP; P01233; 1XUL.
CC GlycoSuiteDB; P01231; -.
CC InterPro; IPR000359; Cys_knot.
CC InterPro; IPR002400; GF_cys_knot.
CC Pfam; PF00007; Cys_knot; 1.
CC PRINTS; P000438; GFCYSKNOT.
CC SMART; SM00068; GH; 1.
CC PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
CC PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
CC Hormone; Signal; Glycoprotein.
FT SIGNAL 1 20 LUTROPIN BETA CHAIN.
FT CHAIN 21 141 BY SIMILARITY.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT MOD_RES 21 21 BLOCKED.
FT CARBOHYD 33 33 N-LINKED (GLCNAC...).
FT VARIANT 138 141 MISSING (IN SOME MOLECULES).
FT CONFLICT 30 30 Q -> E (IN REF. 4).
FT CONFLICT 59 59 L -> P (IN REF. 1).
FT CONFLICT 63 63 R -> Q (IN REF. 2).
FT CONFLICT 71 71 P -> PP (IN REF. 4).
FT CONFLICT 81 81 E -> Q (IN REF. 4).
FT CONFLICT 122 123 GP -> PG (IN REF. 3 AND 4).
FT CONFLICT 126 126 Q -> E (IN REF. 3 AND 4).
SQ SEQUENCE 141 AA; 15184 MW; C59EC7C0AA55A9DC CRC64;

Query Match 55.2%; Score 37; DB 1; Length 141;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 VLPALPQVVC 13
| : : : : :
Db 68 ILPPMPQVVC 77

RESULT 24
LSHB_FELCA STANDARD; PRT; 143 AA.
ID LSHB_FELCA STANDARD; PRT; 143 AA.
AC O77805;
DT 16-OCT-2001 (Rel. 40, Created)

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OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10565;
RN [1]
RP SEQUENCE FROM N.A.
RA Eriksson A.;
RL Submitted (AUG-1987) to the EMBL/GenBank/DBJ databases.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M15953; AAA68660.1; -.
DR FIR; F29499; P2MLEP.
DR InterPro; IPR000784; Late_L2.
DR Pfam; PF00513; Late_protein_L2; 1.
KW Coat protein; Late protein.
SQ SEQUENCE 477 AA; 51250 MW; 15D3A6D4A3B5B366 CRC64;

Query Match 55.2%; Score 37; DB 1; Length 477;
Best Local Similarity 58.3%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 LOGVLPALPQVVC 12
Db 112 LSGILPDAPAVV 123

Search completed: December 4, 2002, 11:26:34
Job time : 8.5 secs

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B).
GN LHB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Pukazhenthi B.S., Varma G.M., Brown J.L.;
RT "Molecular cloning and sequence analysis of the cDNA for the feline
RT luteinizing hormone beta subunit";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF095716; AAC64196.1; -.
DR HSP; P01233; IXOL.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001545; Gly_hormoneb.
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Signal; Glycoprotein.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 143 LUTROPIN BETA CHAIN.
FT DISULFID 31 79 BY SIMILARITY.
FT DISULFID 45 94 BY SIMILARITY.
FT DISULFID 48 132 BY SIMILARITY.
FT DISULFID 56 110 BY SIMILARITY.
FT DISULFID 60 112 BY SIMILARITY.
FT DISULFID 115 122 BY SIMILARITY.
FT CARBOHYD 35 35 N-LINKED GLCNAC... (POTENTIAL).
SQ SEQUENCE 143 AA; 15318 MW; C5C55DDC907422DB CRC64;

Query Match 55.2%; Score 37; DB 1; Length 143;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 1 LOGVLPALPQVVC 13
Db 67 LPAALPPVQVVC 79

RESULT 25
VL2_PAPVE
ID VL2_PAPVE STANDARD; PRT; 477 AA.
AC P11327;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Minor capsid protein L2.
GN L2.
OS European elk papillomavirus (EEPV).

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:24:20 ; Search time 23.075 Seconds
(without alignments)
116.083 Million cell updates/sec

Title: US-09-821-380-2
Perfect score: 67
Sequence: 1 LOGVLPALPQVVC 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	100.0	159	4 Q8WXL4	Q8WXL4 homo sapien
2	67	100.0	159	4 Q8WXL3	Q8WXL3 homo sapien
3	67	100.0	159	4 Q8WXL2	Q8WXL2 homo sapien
4	67	100.0	159	4 Q8WXL1	Q8WXL1 homo sapien
5	67	100.0	159	4 Q8WTL5	Q8WTL5 homo sapien
6	56	83.6	136	6 Q8WXL0	Q8WXL0 homo sapien
7	56	83.6	136	6 Q8WNB8	Q8WNB8 pongo pygma
8	56	83.6	136	6 Q8WNB6	Q8WNB6 presbytis o
9	56	83.6	157	6 Q8WNC7	Q8WNC7 pongo pygma
10	56	83.6	157	6 Q8WNC6	Q8WNC6 pongo pygma
11	56	83.6	157	6 Q8WNC5	Q8WNC5 pongo pygma
12	56	83.6	157	6 Q8WNC4	Q8WNC4 pongo pygma
13	55	82.1	157	6 Q8WNC2	Q8WNC2 presbytis o
14	55	82.1	157	6 Q8WNB9	Q8WNB9 presbytis o
15	53	79.1	159	6 Q8WNB3	Q8WNB3 colobus gue
16	53	79.1	159	6 Q8WNB1	Q8WNB1 colobus gue

17	53	79.1	159	6	Q8WNB0	Q8WNB0 macaca mula
18	53	79.1	159	6	Q8WNA9	Q8WNA9 macaca mula
19	53	79.1	159	6	Q8WBE1	Q8WBE1 macaca fasc
20	49	73.1	156	6	Q8WNA6	Q8WNA6 aotus trivi
21	49	73.1	157	6	Q8WNC3	Q8WNC3 presbytis o
22	49	73.1	157	6	Q8WNC1	Q8WNC1 presbytis o
23	49	73.1	159	6	Q8WNB4	Q8WNB4 colobus gue
24	49	73.1	159	6	Q8WNB2	Q8WNB2 colobus gue
25	49	73.1	159	6	Q8WNA8	Q8WNA8 macaca mula
26	48	71.6	156	6	Q8WNA7	Q8WNA7 callicebus
27	45	67.2	136	6	Q8WNB5	Q8WNB5 colobus gue
28	44	65.7	165	6	Q8GL37	Q8GL37 macaca mula
29	44	65.7	165	11	Q8WNA8	Q8WNA8 mus musculus
30	43	64.2	165	6	Q8WBE2	Q8WBE2 macaca fasc
31	43	64.2	304	10	Q8WNA9	Q8WNA9 arabidopsis
32	43	64.2	2561	11	Q8WIE5	Q8WIE5 mus musculus
33	42	62.7	136	6	Q8WNB7	Q8WNB7 macaca mula
34	42	62.7	444	16	Q8WIL7	Q8WIL7 rhizobium l
35	42	62.7	447	16	Q8WHL4	Q8WHL4 yersinia pe
36	41	61.2	102	5	Q8WXC5	Q8WXC5 caenorhabdi
37	41	61.2	157	6	Q8WNC0	Q8WNC0 presbytis o
38	41	61.2	454	16	Q8WDF1	Q8WDF1 xylella fas
39	41	61.2	771	5	Q19380	Q19380 caenorhabdi
40	40	59.7	184	5	Q8WXC7	Q8WXC7 caenorhabdi
41	40	59.7	240	17	Q8WHL6	Q8WHL6 methanopyru
42	40	59.7	447	4	Q8WNA4	Q8WNA4 homo sapien
43	40	59.7	742	4	Q8WNC2	Q8WNC2 homo sapien
44	40	59.7	795	11	Q8WBY0	Q8WBY0 mus musculus
45	40	59.7	835	4	Q8WCA2	Q8WCA2 homo sapien
46	40	59.7	837	6	Q8WLC2	Q8WLC2 macaca fasc
47	40	59.7	1076	10	Q8WQ50	Q8WQ50 arabidopsis
48	39	58.2	89	16	Q8WHL1	Q8WHL1 bacillus ha
49	39	58.2	105	12	Q8WHL0	Q8WHL0 egyptian su
50	39	58.2	105	12	Q8WXC2	Q8WXC2 egyptian su
51	39	58.2	105	12	Q8WXC8	Q8WXC8 egyptian su
52	39	58.2	105	12	Q8WXC5	Q8WXC5 egyptian su
53	39	58.2	105	12	Q8WHL2	Q8WHL2 egyptian su
54	39	58.2	144	16	Q8WHL1	Q8WHL1 streptomyce
55	39	58.2	271	10	Q8WHL8	Q8WHL8 arabidopsis
56	39	58.2	287	10	Q8WHL2	Q8WHL2 arabidopsis
57	39	58.2	432	16	Q8WHL0	Q8WHL0 rhizobium m
58	39	58.2	482	5	Q8WHL9	Q8WHL9 leishmania
59	39	58.2	526	13	Q8WVC6	Q8WVC6 carassius a
60	39	58.2	1382	10	Q8WHL0	Q8WHL0 oryza sativ
61	39	58.2	1401	10	Q8WHL0	Q8WHL0 arabidopsis
62	39	58.2	1606	10	Q8WHL0	Q8WHL0 arabidopsis
63	38	56.7	154	17	Q8WHL0	Q8WHL0 archaeglob
64	38	56.7	237	4	Q8WHL0	Q8WHL0 homo sapien
65	38	56.7	262	2	Q8WHL0	Q8WHL0 thermus the

ALIGNMENTS

RESULT 1
Q8WXL4 PRELIMINARY; PRT: 159 AA.
ID Q8WXL4
AC Q8WXL4; 2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Rivolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

```

DR EMBL; AF397576; AAL69704.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
DR NON_TER 1 159
FT NON_TER 159
SQ SEQUENCE 159 AA; 16909 MW; A598A73CC97B57EE CRC64;

Query Match 100.0%; Score 67; DB 4; Length 159;
Best Local Similarity 100.0%; Pred.No. 0.00057;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
DB 60 LQGVLPALPQVVC 72

RESULT 2
Q8WXL3 PRELIMINARY; PRT; 159 AA.
AC Q8WXL3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvalo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397578; AAL69706.1; -.
DR InterPro; IPR000359; Cys_knot.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
DR NON_TER 1 159
FT NON_TER 159
SQ SEQUENCE 159 AA; 17006 MW; AFDCA4CE2542EC084 CRC64;

Query Match 100.0%; Score 67; DB 4; Length 159;
Best Local Similarity 100.0%; Pred.No. 0.00057;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
DB 60 LQGVLPALPQVVC 72

RESULT 3
Q8WXL2 PRELIMINARY; PRT; 159 AA.
AC Q8WXL2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (fragment).
GN CGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvalo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397578; AAL69706.1; -.
DR InterPro; IPR000359; Cys_knot.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
DR NON_TER 1 159
FT NON_TER 159
SQ SEQUENCE 159 AA; 17006 MW; AFDCA4CE2542EC084 CRC64;

Query Match 100.0%; Score 67; DB 4; Length 159;
Best Local Similarity 100.0%; Pred.No. 0.00057;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
DB 60 LQGVLPALPQVVC 72

RESULT 5
Q8WTT5 PRELIMINARY; PRT; 159 AA.
ID Q8WTT5
AC Q8WTT5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.

```

RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvalo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF397579; AAL69707.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
DR NON_TER 1 159
FT NON_TER 159
SQ SEQUENCE 159 AA; 16960 MW; 24761E38796A1727 CRC64;

Query Match 100.0%; Score 67; DB 4; Length 159;
Best Local Similarity 100.0%; Pred.No. 0.00057;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
DB 60 LQGVLPALPQVVC 72

RESULT 4

Q8WXL1 PRELIMINARY; PRT; 159 AA.
AC Q8WXL1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvalo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397581; AAL69709.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
DR NON_TER 1 159
FT NON_TER 159
SQ SEQUENCE 159 AA; 16969 MW; 3C963B3C3D2E57FF CRC64;

Query Match 100.0%; Score 67; DB 4; Length 159;
Best Local Similarity 100.0%; Pred.No. 0.00057;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
DB 60 LQGVLPALPQVVC 72

RESULT 5

Q8WTT5 PRELIMINARY; PRT; 159 AA.
ID Q8WTT5
AC Q8WTT5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 RL evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397577; AAL69705.1; -.
 DR EMBL; AF397580; AAL69708.1; -.
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHB; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 159 159
 SQ SEQUENCE 159 AA; 16944 MW; 246BA938796A1727 CRC64;

Query Match 100.0%; Score 67; DB 4; Length 159;
 Best Local Similarity 100.0%; Pred. No. 0.00057;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQVLPALPQVVC 13
 |||||
 Db 60 LQVLPALPQVVC 72

RESULT 6

Q8WXL0
 ID Q8WXL0 PRELIMINARY; PRT; 136 AA.
 AC Q8WXL0;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Luteinizing hormone beta subunit (Fragment).
 GN LHB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 RL evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397591; AAL69719.1; -.
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHB; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 159 159
 SQ SEQUENCE 136 AA; 14712 MW; FE5451852A45054E CRC64;

Query Match 83.6%; Score 56; DB 4; Length 136;
 Best Local Similarity 84.6%; Pred. No. 0.04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQVLPALPQVVC 13
 |||||
 Db 60 LQVLPALPQVVC 72

RESULT 7

Q8WNB8
 ID Q8WNB8 PRELIMINARY; PRT; 136 AA.
 AC Q8WNB8;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Luteinizing hormone beta subunit (Fragment).
 GN LHB.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 RL evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397592; AAL69720.1; -.
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHB; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 159 159
 SQ SEQUENCE 136 AA; 14708 MW; 11F17052CF0DEFB9 CRC64;

Query Match 83.6%; Score 56; DB 6; Length 136;
 Best Local Similarity 84.6%; Pred. No. 0.04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQVLPALPQVVC 13
 |||||
 Db 60 LQVLPALPQVVC 72

RESULT 8

Q8WNB6
 ID Q8WNB6 PRELIMINARY; PRT; 136 AA.
 AC Q8WNB6;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Luteinizing hormone beta subunit (Fragment).
 GN LHB.
 OS Presbytis obscura.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
 OX Presbytis.
 OX NCBI_TaxID=78450;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 RL evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397594; AAL69722.1; -.
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHB; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 159 159
 SQ SEQUENCE 136 AA; 14722 MW; 2EA6300910968492 CRC64;

Query Match 83.6%; Score 56; DB 6; Length 136;
 Best Local Similarity 84.6%; Pred. No. 0.04;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQVLPALPQVVC 13
 |||||
 Db 60 LQVLPALPQVVC 72

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RESULT 9
Q8WNC7
ID Q8WNC7 PRELIMINARY; PRT; 157 AA.
AC Q8WNC7;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397582; AAL69710.1; -.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 16928 MW; 825D27A00EFBD4F6 CRC64;

Query Match 83.6%; Score 56; DB 6; Length 157;
Best Local Similarity 84.6%; Pred. No. 0.046;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQSVLPALPQVVC 13
Db 60 LQSVLPPLPQVVC 72

RESULT 10
Q8WNC6
ID Q8WNC6 PRELIMINARY; PRT; 157 AA.
AC Q8WNC6;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397583; AAL69711.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 16868 MW; 97BD27A014E1D4EC CRC64;

Query Match 83.6%; Score 56; DB 6; Length 157;
Best Local Similarity 84.6%; Pred. No. 0.046;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 LQSVLPALPQVVC 13
Db 60 LQSVLPPLPQVVC 72

RESULT 11
Q8WNC5
ID Q8WNC5 PRELIMINARY; PRT; 157 AA.
AC Q8WNC5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397584; AAL69712.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 17027 MW; 8317774E0F4BD4ED CRC64;

Query Match 83.6%; Score 56; DB 6; Length 157;
Best Local Similarity 84.6%; Pred. No. 0.046;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQSVLPALPQVVC 13
Db 60 LQSVLPPLPQVVC 72

RESULT 12
Q8WNC4
ID Q8WNC4 PRELIMINARY; PRT; 157 AA.
AC Q8WNC4;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397585; AAL69713.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 16985 MW; 825D27AC3EFD4F6 CRC64;
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Query Match 83.6%; Score 56; DB 6; Length 157;
Best Local Similarity 84.6%; Pred. No. 0.046;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
DB 60 LQGVLPALPQVVC 72

RESULT 13
Q8WNC2 ID Q8WNC2 PRELIMINARY; PRT; 157 AA.
AC Q8WNC2;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Presbytis obscura.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Presbytis.
OX NCBI_TaxID=78450;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an evolutionary history of selection."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397587; AAL69715.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 16773 MW; 17F1B4E17BE57CB3 CRC64;

Query Match 82.1%; Score 55; DB 6; Length 157;
Best Local Similarity 76.9%; Pred. No. 0.068;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
DB 60 LQGVLPALPQVVC 72

RESULT 14
Q8WNB9 ID Q8WNB9 PRELIMINARY; PRT; 157 AA.
AC Q8WNB9;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Presbytis obscura.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Presbytis.
OX NCBI_TaxID=78450;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an evolutionary history of selection."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397590; AAL69718.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.

DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 16787 MW; EDF14B8C3B88C7B3 CRC64;

Query Match 82.1%; Score 55; DB 6; Length 157;
Best Local Similarity 76.9%; Pred. No. 0.068;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
DB 60 LQGVLPALPQVVC 72

RESULT 15
Q8WNB3 ID Q8WNB3 PRELIMINARY; PRT; 159 AA.
AC Q8WNB3;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Colobus quereza (Black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Colobus.
OX NCBI_TaxID=33548;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an evolutionary history of selection."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397597; AAL69725.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA; 16942 MW; 26F692957BD09E35 CRC64;

Query Match 79.1%; Score 53; DB 6; Length 159;
Best Local Similarity 76.9%; Pred. No. 0.15;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
DB 60 LQGVLPALPQVVC 72

RESULT 16
Q8WNB1 ID Q8WNB1 PRELIMINARY; PRT; 159 AA.
AC Q8WNB1;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Colobus quereza (Black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Colobus.
OX NCBI_TaxID=33548;
RN [1]
RP SEQUENCE FROM N.A.

RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF397599; AAL69727.1; -.
 DR InterPro: IPR000359; Cys_knot.
 DR InterPro: IPR001545; Gly_hormoneB.
 DR Pfam: PF00007; Cys_knot; 1.
 DR SMART: SM00068; GHB; 1.
 DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 159
 SQ SEQUENCE 159 AA; 17012 MW; 367EDDDCDE7F6005 CRC64;

Query Match 79.1%; Score 53; DB 6; Length 159;
 Best Local Similarity 76.9%; Pred. No. 0.15;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGVLPALPQVVC 13
 II III :IIII
 Db 60 LQAVLPVPQVVC 72

RESULT 17

Q8WNB0 PRELIMINARY; PRT; 159 AA.
 ID Q8WNB0;
 AC Q8WNB0;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Chorionic gonadotropin beta subunit (Fragment).
 GN CGB.

OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF397600; AAL69728.1; -.
 DR InterPro: IPR000359; Cys_knot.
 DR InterPro: IPR001545; Gly_hormoneB.
 DR Pfam: PF00007; Cys_knot; 1.
 DR SMART: SM00068; GHB; 1.
 DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 159
 SQ SEQUENCE 159 AA; 16853 MW; 7B64051C2F863870 CRC64;

Query Match 79.1%; Score 53; DB 6; Length 159;
 Best Local Similarity 76.9%; Pred. No. 0.15;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGVLPALPQVVC 13
 II III :IIII
 Db 60 LQAVLPVPQVVC 72

RESULT 18

Q8WNA9 PRELIMINARY; PRT; 159 AA.
 ID Q8WNA9;
 AC Q8WNA9;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Chorionic gonadotropin beta subunit (Fragment).
 GN CGB.

OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF397601; AAL69729.1; -.
 DR InterPro: IPR000359; Cys_knot.
 DR InterPro: IPR001545; Gly_hormoneB.
 DR Pfam: PF00007; Cys_knot; 1.
 DR SMART: SM00068; GHB; 1.
 DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 159
 SQ SEQUENCE 159 AA; 16915 MW; 9231691ED0D82863 CRC64;

Query Match 79.1%; Score 53; DB 6; Length 159;
 Best Local Similarity 76.9%; Pred. No. 0.15;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGVLPALPQVVC 13
 II III :IIII
 Db 60 LQAVLPVPQVVC 72

RESULT 19

Q9BEH1 PRELIMINARY; PRT; 165 AA.
 ID Q9BEH1;
 AC Q9BEH1;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Chorionic gonadotropin beta subunit 2.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE-EMBRYONIC TROPHOBLAST;
 RA Wilken J.A., Matsumoto K., Lasley B.L., Bedows E.;
 RT "A Comparison of Chorionic Gonadotropin Expression by Human and
 Macaque Trophoblast Cells."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY026360; AAK08644.1; -.
 DR HSSP: P01233; 1XUL.
 DR InterPro: IPR000359; Cys_knot.
 DR InterPro: IPR001545; Gly_hormoneB.
 DR Pfam: PF00007; Cys_knot; 1.
 DR SMART: SM00068; GHB; 1.
 DR PROSITE: PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE: PS00689; GLYCO_HORMONE_BETA_2; 1.
 SQ SEQUENCE 165 AA; 17743 MW; 2F21566B48592471 CRC64;

Query Match 79.1%; Score 53; DB 6; Length 165;
 Best Local Similarity 76.9%; Pred. No. 0.16;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LGVLPALPQVVC 13
 II III :IIII
 Db 65 LQAVLPVPQVVC 77

RESULT 20

Q8WNA6 PRELIMINARY; PRT; 156 AA.
 ID Q8WNA6

Db 60 LQAVLPVPQAVC 72

RESULT 22

Q8WNC1 PRELIMINARY; PRT; 157 AA.

AC Q8WNC1;

DT 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE Chorionic gonadotropin beta subunit (Fragment).

DE CGB.

OS Presbytis obscura.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;

OC Presbytis.

OX NCBI_TaxID=78450;

RN [1]

RA SEQUENCE FROM N.A.

RA Maston G.A., Ruvolo M.;

RT "Chorionic gonadotropin has a recent origin in primates and an evolutionary history of selection.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF397588; AAL69716.1; -.

DR InterPro; IPR000359; Cys_Knot.

DR InterPro; IPR001545; Gly_hormoneB.

DR Pfam; PF00007; Cys_Knot; 1.

DR SMART; SM00068; GHB; 1.

DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.

DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.

FT NON_TER 1

FT NON_TER 157

FT NON_TER 157

SQ SEQUENCE 157 AA; 16745 MW; 1D49080831C14F0C CRC64;

Query Match 73.18; Score 49; DB 6; Length 157;

Best Local Similarity 69.28; Pred. No. 0.75;

Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps

QY 1 LQGLPALPQVVC 13

|| ||| :|| ||

Db 60 LQAVLPVPQAVC 72

RESULT 23

Q8WNB4 PRELIMINARY; PRT; 159 AA.

AC Q8WNB4;

DT 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE Chorionic gonadotropin beta subunit (Fragment).

DE CGB.

OS Colobus guereza (Black-and-white colobus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;

OC Colobus.

OX NCBI_TaxID=33548;

RN [1]

RA SEQUENCE FROM N.A.

RA Maston G.A., Ruvolo M.;

RT "Chorionic gonadotropin has a recent origin in primates and an evolutionary history of selection.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL; AF397596; AAL69724.1; -.

DR InterPro; IPR000359; Cys_Knot.

DR InterPro; IPR001545; Gly_hormoneB.

DR Pfam; PF00007; Cys_Knot; 1.

DR SMART; SM00068; GHB; 1.

DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.

DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.

FT NON_TER 1

FT NON_TER 159

SQ SEQUENCE 159 AA; 16904 MW; 71C31ADD81986B01 CRC64;

```
Query Match      73.1%; Score 49; DB 6; Length 159;
Best Local Similarity 69.2%; Pred. No. 0.76;
Matches 9; Conservative 1; Mismatches 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
   |||||:||||
Db 60 LQAVLPVPQAVC 72

RESULT 24
Q8WNB2 PRELIMINARY; PRT; 159 AA.
AC Q8WNB2;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Colobus guereza (Black-and-white colobus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae;
OC Colobus.
OX NCBI_TaxID=33548;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
RL evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397598; AAL69726.1; -
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 159
FT NON_TER 159
SQ SEQUENCE 159 AA; 16972 MW; 725BA76BC2887660 CRC64;

Query Match      73.1%; Score 49; DB 6; Length 159;
Best Local Similarity 69.2%; Pred. No. 0.76;
Matches 9; Conservative 1; Mismatches 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
   |||||:||||
Db 60 LQAVLPVPQAVC 72

RESULT 25
Q8WNB2 PRELIMINARY; PRT; 159 AA.
AC Q8WNB2;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
RL evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397602; AAL69730.1; -
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
```

```
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 159
FT NON_TER 159
SQ SEQUENCE 159 AA; 17032 MW; 726E29F7A27E5C04 CRC64;

Query Match      73.1%; Score 49; DB 6; Length 159;
Best Local Similarity 69.2%; Pred. No. 0.76;
Matches 9; Conservative 2; Mismatches 0; Gaps 0;

QY 1 LQGVLPALPQVVC 13
   |||||:||||
Db 60 LQVILPPVPQVVC 72

Search completed: December 4, 2002, 11:28:34
Job time : 25.075 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:21:04 ; Search time 22.25 Seconds
(without alignments)
59.888 Million cell updates/sec

Title: US-09-821-380-3
Perfect score: 52
Sequence: 1 VLPALPQVVC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database :

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22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	22	AAU08738 Human immunoregula
2	52	100.0	11	19	AAW47499 Human beta-hCG pro
3	52	100.0	11	19	AAW50094 Human chorionic go
4	52	100.0	11	19	AAW50059 Human chorionic go
5	52	100.0	12	19	AAW47493 Human beta-hCG pro
6	52	100.0	12	19	AAW50088 Human chorionic go
7	52	100.0	12	19	AAW50053 Human chorionic go
8	52	100.0	13	19	AAW47477 Human beta-hCG pro
9	52	100.0	13	19	AAW50037 Human chorionic go
10	52	100.0	13	19	AAW50072 Human chorionic go

11	52	100.0	13	22	AAU08737 Human immunoregula
12	52	100.0	13	22	AAW71783 Beta-human chorion
13	52	100.0	13	23	AAU83032 Human Satellin A1
14	52	100.0	14	19	AAW47489 Human beta-hCG pro
15	52	100.0	14	19	AAW47497 Human beta-hCG pro
16	52	100.0	14	19	AAW47483 Human beta-hCG pro
17	52	100.0	14	19	AAW50043 Human chorionic go
18	52	100.0	14	19	AAW50092 Human chorionic go
19	52	100.0	14	19	AAW50084 Human chorionic go
20	52	100.0	14	19	AAW50078 Human chorionic go
21	52	100.0	14	19	AAW50049 Human chorionic go
22	52	100.0	14	19	AAW50057 Human chorionic go
23	52	100.0	14	22	AAW71784 Beta-human chorion
24	52	100.0	14	22	AAW71804 Beta-hCG Satellin
25	52	100.0	14	23	AAU83033 Human Satellin A2
26	52	100.0	15	19	AAW47508 Human beta-hCG scr
27	52	100.0	15	19	AAW50068 Human chorionic go
28	52	100.0	15	19	AAW50103 Human chorionic go
29	52	100.0	17	17	AAW15308 Human chorionic go
30	52	100.0	17	22	AAU08736 Human immunoregula
31	52	100.0	20	10	AAW91856 38-57 region of hu
32	52	100.0	20	10	AAW90568 Peptide similar to
33	52	100.0	20	19	AAW69468 HCG antigenic pept
34	52	100.0	20	19	AAW47505 Human beta-hCG pro
35	52	100.0	20	19	AAW50100 Human chorionic go
36	52	100.0	20	19	AAW50065 Human chorionic go
37	52	100.0	20	20	AAW93453 Human hCG beta-sub
38	52	100.0	20	21	AAW15353 Human chorionic go
39	52	100.0	20	22	AAU02856 Peptide containing
40	52	100.0	20	22	AAU02871 Human Chorionic Go
41	52	100.0	20	22	AAU02875 Human Chorionic Go
42	52	100.0	20	22	AAU01158 Structure xxvii (p
43	52	100.0	20	22	AAW49904 Human chorionic go
44	52	100.0	22	8	AAW71013 Sequence of fragme
45	52	100.0	23	19	AAW47502 Human beta-hCG pro
46	52	100.0	23	19	AAW50097 Human chorionic go
47	52	100.0	23	19	AAW50098 Human chorionic go
48	52	100.0	23	19	AAW50062 Human chorionic go
49	52	100.0	23	19	AAW50063 Human chorionic go
50	52	100.0	24	19	AAW47501 Human beta-hCG pro
51	52	100.0	24	19	AAW50096 Human chorionic go
52	52	100.0	24	19	AAW50061 Human chorionic go
53	52	100.0	24	22	AAW64086 Human Clara cell p
54	52	100.0	25	22	AAW64108 Human Clara cell p
55	52	100.0	27	22	AAU01181 Human chorionic go
56	52	100.0	60	10	AAW91836 Beta subunit of hu
57	52	100.0	85	20	AAW95536 Human chorionic go
58	52	100.0	93	22	AAU04621 Human chorionic go
59	52	100.0	93	22	AAE04493 Human chorionic go
60	52	100.0	98	19	AAW47494 Human beta-hCG pro
61	52	100.0	98	19	AAW50089 Human chorionic go
62	52	100.0	98	19	AAW50054 Human chorionic go
63	52	100.0	111	12	AAW15161 hCG deletion mutan
64	52	100.0	114	14	AAW31003 Modified hCG beta-
65	52	100.0	114	14	AAW31005 Modified hCG beta-

ALIGNMENTS

RESULT 1
AAU08738
ID AAU08738 standard; Peptide: 10 AA.
XX
AC AAU08738;
XX
DT 19-DEC-2001 (first entry)
XX
DE Human immunoregulator functional fragment peptide #3.
DE
XX Immunoregulator; human; beta-human chorionic gonadotropin; beta-hCG;
KW inflammation; multiple sclerosis; diabetes; anaphylactic shock; asthma;
KW pregnancy related disorder; pre-eclampsia; autoimmune disease; allergy;
KW

KW rheumatoid arthritis; Sjogren's syndrome; graft-versus-host disease;
 KW thrombocytopenia; pernicious anaemia; Addison's disease; dermatomyositis;
 KW idiopathic leucopenia; primary biliary cirrhosis; cryptogenic cirrhosis;
 KW active chronic hepatitis; ulcerative colitis; polyomyelitis; scleroderma;
 KW mixed connective tissue disease; discoid lupus erythematosus; neutropenic;
 KW antidiabetic; immunosuppressive; dermatological; antirheumatic; virucide;
 KW antiarthritic; antiasthmatic; anti-infertility; haemostatic;
 KW antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 PN EP1138692-A1.
 XX
 PD 04-OCT-2001.
 XX
 XX 29-MAR-2000; 2000EP-0201139.
 PF
 XX 29-MAR-2000; 2000EP-0201139.
 PR
 XX (UYRO-) UNIV ROTTERDAM ERASMUS.
 PA
 XX Khan NA, Benner R;
 XX WPI; 2001-627804/73.
 XX
 XX Immunoregulator useful in the treatment of e.g. diabetes is obtained or
 PT derived from nicked beta-human chorionic gonadotropin -
 PT
 XX Claim 7; Page 19; 36pp; English.
 PS
 XX The invention relates to an immunoregulator obtained or derived from
 CC nicked beta-human chorionic gonadotropin (beta-hCG). The immunoregulator
 CC can be used in the treatment of immune-mediated disorders such as chronic
 CC inflammation (e.g. multiple sclerosis, diabetes), acute inflammation
 CC (e.g. septic or anaphylactic shock), pregnancy related immune-mediated
 CC disorders (e.g. pre-eclampsia), autoimmune disease (e.g. rheumatoid
 CC arthritis), allergy (e.g. asthma), Sjogren's syndrome, graft-versus-host
 CC disease, thrombocytopenia, pernicious anaemia, Addison's disease,
 CC idiopathic leucopenia, primary biliary cirrhosis, active chronic
 CC hepatitis, cryptogenic cirrhosis, ulcerative colitis, dermatomyositis,
 CC polymyositis, scleroderma, mixed connective tissue disease and discoid
 CC lupus erythematosus. This sequence represents a human immunoregulator
 CC functional fragment peptide.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 52; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.017; 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Caps 0;
 QY 1 VLPALPQVVC 10
 DB 1 VLPALPQVVC 10
 |||||
 RESULT 2
 AAW47499
 ID AAW47499 standard; Protein; 11 AA.
 XX
 AC AAW47499;
 XX
 XX 23-SEP-1998 (first entry)
 DT
 XX Human beta-hCG protein fragment (aa 47-57).
 DE
 XX Beta-human chorionic gonadotropin; beta-hCG; hematopoiesic cell; HIV;
 KW treatment; proliferation; human immunodeficiency virus; disulphide;
 KW idiopathic thrombocytopenia purpura; anaemia; neutropenia; tumour;
 KW chemotherapy; radiation; autoimmune disease; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO9749418-A1.

XX 31-DEC-1997.
 PD
 XX 24-JUN-1997; 97WO-US11209.
 PF
 XX 09-SEP-1996; 96US-0709924.
 PR
 XX 24-JUN-1996; 96US-0669654.
 XX
 PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 XX
 XX Bryant J, Gallo RC, Lunardi-Iskandar Y;
 PI
 XX WPI; 1998-076906/07.
 DR
 XX
 XX Treating or preventing disease by increasing production of
 PT haematopoietic cells - using human chorionic gonadotropin or its
 PT fragments or derivatives, in vivo or in vitro, e.g. in cases of HIV
 PT infection, anaemia etc.
 XX
 PS Claim 9; Page 98; 162pp; English.
 XX
 CC AAW47474-W47508 represent fragments of the beta subunit of human
 CC chorionic gonadotropin which is used in a method for the treatment or
 CC prevention of disease, by increasing production of at least one type of
 CC haematopoietic cell. A method is also described in which non-terminally
 CC differentiated haematopoietic cells are treated in vitro to increase
 CC proliferation then returned to the patient. The method is specified for
 CC treating human immunodeficiency virus (HIV) infection, idiopathic
 CC thrombocytopenia purpura, anaemia or neutropenia, or subjects who have
 CC undergone chemotherapy or radiation treatment. More generally it can be
 CC used to treat a wide range of conditions involving haematopoietic
 CC failure, (non-) haematopoietic tumours, autoimmune disease and genetic
 CC disorders (using a transformed haematopoietic cell). The in vitro method
 CC can also be used to expand haematopoietic cells for subsequent
 CC therapeutic use.
 XX
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 52; DB 19; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLPALPQVVC 10
 DB 2 VLPALPQVVC 11
 |||||
 RESULT 3
 AAW50094
 ID AAW50094 standard; peptide; 11 AA.
 XX
 AC AAW50094;
 XX
 XX 26-JUN-1998 (first entry)
 DT
 XX Human chorionic gonadotropin beta-chain fragment.
 DE
 XX Beta-chain; human; chorionic gonadotropin; beta-hCG; treatment;
 KW prevention; wasting syndrome; viral infection; cancer;
 KW chronic cardiovascular disease; chemotherapy;
 KW radiation therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9749721-A1.
 XX
 PD 31-DEC-1997.
 XX
 PF 24-JUN-1997; 97WO-US11448.
 XX
 XX 09-SEP-1996; 96US-0709933.
 PR
 XX 24-JUN-1996; 96US-0669675.
 XX

PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 XX Bryant J, Gallo RC, Lunardi-Iskandar Y;
 XX WPI; 1998-077106/07.
 XX
 XX Treating or preventing wasting syndrome - by administration of human
 PT chorionic gonadotropin, beta-hCG, peptides or derivatives of these
 XX
 XX Claim 10; Page 77; 126pp; English.
 XX
 XX The present sequence is a peptide derivative of the beta-chain of
 CC human chorionic gonadotropin (beta-hCG). The peptide can be used
 CC to treat or prevent a wasting syndrome associated with viral
 CC infection, e.g. human immunodeficiency syndrome virus infection,
 CC cancer, chronic cardiovascular disease, chemotherapy or radiation
 CC therapy.
 XX
 XX Sequence 11 AA;
 SQ

Query Match 100.0%; Score 52; DB 19; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
 Db 2 VLPALPQVVC 11
 |||||

RESULT 4
 AAW50059
 ID AAW50059 standard; peptide; 11 AA.
 XX
 XX AAW50059;
 AC
 XX
 XX 26-JUN-1998 (first entry)
 DT
 XX
 XX Human chorionic gonadotropin beta-chain fragment.
 DE
 XX Beta-chain; human; chorionic gonadotropin; beta-hCG; inhibition;
 KW human immunodeficiency virus; HIV; infection; replication;
 KW Kaposi's sarcoma; haematopoiesis.
 XX
 XX Homo sapiens.
 OS
 XX WO9749373-A2.
 PN
 XX
 XX 31-DEC-1997.
 PD
 XX
 XX 24-JUN-1997; 97WO-US11202.
 PF
 XX
 XX 09-SEP-1996; 96US-0709948.
 PR
 XX 24-JUN-1996; 96US-0669681.
 XX
 XX (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 PA
 XX Bryant J, Gallo RC, Lunardi-Iskandar Y;
 PI WPI; 1998-076887/07.
 XX
 XX Human chorionic gonadotropin peptide derivatives - are active in
 DR inhibiting, e.g. HIV infection or replication, Kaposi's Sarcoma or
 XX have pro-haematopoietic activity
 XX
 XX Claim 6; Page 109; 174pp; English.
 PS
 XX The present sequence is a peptide derivative of the beta-chain of
 CC human chorionic gonadotropin (beta-hCG). The peptide is active in
 CC inhibiting, e.g. HIV infection or replication or Kaposi's sarcoma,
 CC or has pro-haematopoietic activity.
 XX
 XX Sequence 11 AA;
 SQ

Query Match 100.0%; Score 52; DB 19; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
 Db 2 VLPALPQVVC 11
 |||||

RESULT 5
 AAW47493
 ID AAW47493 standard; Protein; 12 AA.
 XX
 XX AAW47493;
 AC
 XX 23-SEP-1998 (first entry)
 DT
 XX
 XX Human beta-hCG protein fragment (aa 47-58).
 DE
 XX
 XX Beta-human chorionic gonadotropin; beta-hCG; hematopoietic cell;
 KW treatment; proliferation; human immunodeficiency virus; HIV; tumour;
 KW idiopathic thrombocytopenia purpura; anaemia; neutropaenia;
 KW chemotherapy; radiation; autoimmune disease; genetic disorder.
 XX
 XX Homo sapiens.
 OS
 XX WO9749418-A1.
 PN
 XX
 XX 31-DEC-1997.
 PD
 XX
 XX 24-JUN-1997; 97WO-US11209.
 PF
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 XX 09-SEP-1996; 96US-0709924.
 PR
 XX 24-JUN-1996; 96US-0669654.
 XX
 XX (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 PA
 XX Bryant J, Gallo RC, Lunardi-Iskandar Y;
 PI WPI; 1998-076906/07.
 XX
 XX Treating or preventing disease by increasing production of
 PT haematopoietic cells - using human chorionic gonadotropin or its
 PT fragments or derivatives, in vivo or in vitro, e.g. in cases of HIV
 PT infection, anaemia etc.
 XX
 XX Claim 7; Page 96; 162pp; English.
 PS
 XX
 XX AAW47474-W47508 represent fragments of the beta subunit of human
 CC chorionic gonadotropin which is used in a method for the treatment or
 CC prevention of disease, by increasing production of at least one type of
 CC haematopoietic cell. A method is also described in which non-terminally
 CC differentiated haematopoietic cells are treated in vitro to increase
 CC proliferation then returned to the patient. The method is specified for
 CC treating human immunodeficiency virus (HIV) infection, idiopathic
 CC thrombocytopenia purpura, anaemia or neutropaenia, or subjects who have
 CC undergone chemotherapy or radiation treatment. More generally it can be
 CC used to treat a wide range of conditions involving haematopoietic
 CC failure, (non-) haematopoietic tumours, autoimmune disease and genetic
 CC disorders (using a transformed haematopoietic cell). The in vitro method
 CC can also be used to expand haematopoietic cells for subsequent
 CC therapeutic use.
 XX
 XX Sequence 12 AA;
 SQ

```
RESULT 6
AAW50088
ID AAW50088 standard; peptide; 12 AA.
XX
AC AAW50088;
XX
DT 26-JUN-1998 (first entry)
XX
DE Human chorionic gonadotrophin beta-chain fragment.
XX
KW Beta-chain; human; chorionic gonadotrophin; beta-hCG; treatment;
KW prevention; wasting syndrome; viral infection; cancer;
KW chronic cardiovascular disease; chemotherapy;
KW radiation therapy.
XX
OS Homo sapiens.
XX
PN WO9749721-A1.
XX
PD 31-DEC-1997.
XX
PF 24-JUN-1997; 97WO-US11448.
XX
PR 09-SEP-1996; 96US-0709933.
XX
PR 24-JUN-1996; 96US-0669675.
XX
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
PI Bryant J, Gallo RC, Lunardi-Iskandar Y;
XX
XX WPI; 1998-077106/07.
XX
XX Treating or preventing wasting syndrome - by administration of human
XX chorionic gonadotrophin, beta-hCG, peptides or derivatives of these
XX
XX Claim 8; Page 75; 126pp; English.
XX
XX The present sequence is a peptide derivative of the beta-chain of
XX human chorionic gonadotrophin (beta-hCG). The peptide can be used
XX to treat or prevent a wasting syndrome associated with viral
XX infection, e.g. human immunodeficiency syndrome virus infection,
XX cancer, chronic cardiovascular disease, chemotherapy or radiation
XX therapy.
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 52; DB 19; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 2 VLPALPQVVC 11
|||||
|

RESULT 7
AAW50053
ID AAW50053 standard; peptide; 12 AA.
XX
AC AAW50053;
XX
DT 26-JUN-1998 (first entry)
XX
DE Human chorionic gonadotrophin beta-chain fragment.
XX
KW Beta-chain; human; chorionic gonadotrophin; beta-hCG; inhibition;
KW human immunodeficiency virus; HIV; infection; replication;
KW Kaposi's sarcoma; haematopoiesis.
XX
OS Homo sapiens.
XX
PN WO9749373-A2.
XX

RESULT 8
AAW47477
ID AAW47477 standard; Protein; 13 AA.
XX
AC AAW47477;
XX
DT 23-SEP-1998 (first entry)
XX
DE Human beta-hCG protein fragment (aa 45-57).
XX
KW Beta-human chorionic gonadotrophin; beta-hCG; hematopoietic cell;
KW treatment; proliferation; human immunodeficiency virus; HIV; tumour;
KW idiopathic thrombocytopenia purpura; anaemia; neutropenia;
KW chemotherapy; radiation; autoimmune disease; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO9749418-A1.
XX
PD 31-DEC-1997.
XX
PF 24-JUN-1997; 97WO-US11209.
XX
PR 09-SEP-1996; 96US-0709924.
XX
PR 24-JUN-1996; 96US-0669654.
XX
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
PI Bryant J, Gallo RC, Lunardi-Iskandar Y;
XX
XX WPI; 1998-076906/07.
XX
XX Treating or preventing disease by increasing production of
XX haematopoietic cells - using human chorionic gonadotrophin or its
XX fragments or derivatives, in vivo or in vitro, e.g. in cases of HIV
XX infection, anaemia etc.
XX
```

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XX
PD 31-DEC-1997.
XX
PF 24-JUN-1997; 97WO-US11202.
XX
PR 09-SEP-1996; 96US-0709948.
XX
PR 24-JUN-1996; 96US-0669681.
XX
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
PI Bryant J, Gallo RC, Lunardi-Iskandar Y;
XX
XX WPI; 1998-076887/07.
XX
XX Human chorionic gonadotrophin peptide derivatives - are active in
XX inhibiting, e.g. HIV infection or replication, Kaposi's Sarcoma or
XX have pro-haematopoietic activity
XX
XX Claim 1; Page 107; 174pp; English.
XX
XX The present sequence is a peptide derivative of the beta-chain of
XX human chorionic gonadotrophin (beta-hCG). The peptide is active in
XX inhibiting, e.g. HIV infection or replication or Kaposi's sarcoma,
XX or has pro-haematopoietic activity.
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 52; DB 19; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 2 VLPALPQVVC 11
|||||
|

RESULT 8
AAW47477
ID AAW47477 standard; Protein; 13 AA.
XX
AC AAW47477;
XX
DT 23-SEP-1998 (first entry)
XX
DE Human beta-hCG protein fragment (aa 45-57).
XX
KW Beta-human chorionic gonadotrophin; beta-hCG; hematopoietic cell;
KW treatment; proliferation; human immunodeficiency virus; HIV; tumour;
KW idiopathic thrombocytopenia purpura; anaemia; neutropenia;
KW chemotherapy; radiation; autoimmune disease; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO9749418-A1.
XX
PD 31-DEC-1997.
XX
PF 24-JUN-1997; 97WO-US11209.
XX
PR 09-SEP-1996; 96US-0709924.
XX
PR 24-JUN-1996; 96US-0669654.
XX
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
PI Bryant J, Gallo RC, Lunardi-Iskandar Y;
XX
XX WPI; 1998-076906/07.
XX
XX Treating or preventing disease by increasing production of
XX haematopoietic cells - using human chorionic gonadotrophin or its
XX fragments or derivatives, in vivo or in vitro, e.g. in cases of HIV
XX infection, anaemia etc.
XX
```


PS Claim 7; Page 92; 162pp; English.

CC AAW47474-W47508 represent fragments of the beta subunit of human

CC chorionic gonadotropin which is used in a method for the treatment or

CC prevention of disease, by increasing production of at least one type of

CC haematopoietic cell. A method is also described in which non-terminally

CC differentiated haematopoietic cells are treated in vitro to increase

CC proliferation then returned to the patient. The method is specified for

CC treating human immunodeficiency virus (HIV) infection, idiopathic

CC thrombocytopaenia purpura, anaemia or neutropenia, or subjects who have

CC undergone chemotherapy or radiation treatment. More generally it can be

CC used to treat a wide range of conditions involving haematopoietic

CC failure. (non-) haematopoietic tumours, autoimmune disease and genetic

CC disorders (using a transformed haematopoietic cell). The in vitro method

CC can also be used to expand haematopoietic cells for subsequent

CC therapeutic use.

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 52; DB 19; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.022;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10

Db ||||||

4 VLPALPQVVC 13

RESULT 9

AAW50037

ID AAW50037 standard; peptide; 13 AA.

XX

AC AAW50037;

XX

DT 26-JUN-1998 (first entry)

XX

DE Human chorionic gonadotropin beta-chain fragment.

XX

KW Beta-chain; human; chorionic gonadotropin; beta-hCG; inhibition;

KW human immunodeficiency virus; HIV; infection; replication;

KW Kaposi's sarcoma; haematopoiesis.

XX

OS Homo sapiens.

XX

PN WO9749373-A2.

XX

PD 31-DEC-1997.

XX

PF 24-JUN-1997; 97WO-US11202.

XX

PR 09-SEP-1996; 96US-0709948.

XX

PR 24-JUN-1996; 96US-0669681.

XX

PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX

PI Bryant J, Gallo RC, Lunardi-Iskandar Y;

XX

XX WPI; 1998-076887/07.

XX

PT Human chorionic gonadotropin peptide derivatives - are active in

PT inhibiting, e.g. HIV infection or replication, Kaposi's Sarcoma or

PT have pro-haematopoietic activity

XX

PS Claim 6; Page 103; 174pp; English.

XX

XX The present sequence is a peptide derivative of the beta-chain of

CC human chorionic gonadotropin (beta-hCG). The peptide is active in

CC inhibiting, e.g. HIV infection or replication or Kaposi's sarcoma,

CC or has pro-haematopoietic activity.

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 52; DB 19; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.022;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10

Db ||||||

4 VLPALPQVVC 13

RESULT 11

AAU08737

ID AAU08737 standard; Peptide; 13 AA.

XX

AC AAU08737;

XX

DT 19-DEC-2001 (first entry)

XX

DE Human immunoregulator functional fragment peptide #2.

XX

Best Local Similarity 100.0%; Pred. No. 0.022;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10

Db ||||||

4 VLPALPQVVC 13

RESULT 10

AAW50072

ID AAW50072 standard; peptide; 13 AA.

XX

AC AAW50072;

XX

DT 26-JUN-1998 (first entry)

XX

DE Human chorionic gonadotropin beta-chain fragment.

XX

KW Beta-chain; human; chorionic gonadotropin; beta-hCG; treatment;

KW prevention; wasting syndrome; viral infection; cancer;

KW chronic cardiovascular disease; chemotherapy;

KW radiation therapy.

XX

OS Homo sapiens.

XX

PN WO9749721-A1.

XX

PD 31-DEC-1997.

XX

PF 24-JUN-1997; 97WO-US11448.

XX

PR 09-SEP-1996; 96US-0709933.

XX

PR 24-JUN-1996; 96US-0669675.

XX

PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX

PI Bryant J, Gallo RC, Lunardi-Iskandar Y;

XX

XX WPI; 1998-077106/07.

XX

PT Treating or preventing wasting syndrome - by administration of human

PT chorionic gonadotropin, beta-hCG, peptides or derivatives of these

XX

PS Claim 8; Page 71; 126pp; English.

XX

CC The present sequence is a peptide derivative of the beta-chain of

CC human chorionic gonadotropin (beta-hCG). The peptide can be used

CC to treat or prevent a wasting syndrome associated with viral

CC infection, e.g. human immunodeficiency syndrome virus infection,

CC cancer, chronic cardiovascular disease, chemotherapy or radiation

CC therapy.

XX

SQ Sequence 13 AA;

Query Match 100.0%; Score 52; DB 19; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.022;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10

Db ||||||

4 VLPALPQVVC 13

KW Immunoregulator; human; beta-human chorionic gonadotropin; beta-HCG;
 KW inflammation; multiple sclerosis; diabetes; anaphylactic shock; asthma;
 KW pregnancy related disorder; pre-eclampsia; autoimmune disease; allergy;
 KW rheumatoid arthritis; Sjogren's syndrome; graft-versus-host disease;
 KW thrombocytopenia; pernicious anaemia; Addison's disease; dermatomyositis;
 KW idiopathic leucopenia; primary biliary cirrhosis; cryptogenic cirrhosis;
 KW active chronic hepatitis; ulcerative colitis; polymyositis; scleroderma;
 KW mixed connective tissue disease; discoid lupus erythematosus; neutropenic;
 KW antidiabetic; immunosuppressive; dermatological; antirheumatic; virucide;
 KW antiarthritic; antiasthmatic; anti-infertility; haemostatic;
 KW antiinflammatory.

XX Homo sapiens.

XX OS

XX PN EPI138692-A1.

XX PD 04-OCT-2001.

XX XX 29-MAR-2000; 2000EP-0201139.

XX PF 29-MAR-2000; 2000EP-0201139.

XX PR (UYRO-) UNIV ROTTERDAM ERASMUS.

XX PA Khan NA, Benner R;

XX PI WPI; 2001-627804/73.

XX DR Immunoregulator useful in the treatment of e.g. diabetes is obtained or
 XX PT derived from nicked beta-human chorionic gonadotropin -
 XX PS Claim 6; Page 18; 36pp; English.

XX The invention relates to an immunoregulator obtained or derived from
 CC nicked beta-human chorionic gonadotropin (beta-HCG). The immunoregulator
 CC can be used in the treatment of immune-mediated disorders such as chronic
 CC inflammation (e.g. multiple sclerosis, diabetes), acute inflammation
 CC (e.g. septic or anaphylactic shock), pregnancy related immune-mediated
 CC disorders (e.g. pre-eclampsia), autoimmune disease (e.g. rheumatoid
 CC arthritis), allergy (e.g. asthma), Sjogren's syndrome, graft-versus-host
 CC disease, thrombocytopenia, pernicious anaemia, Addison's disease,
 CC idiopathic leucopenia, primary biliary cirrhosis, active chronic
 CC hepatitis, cryptogenic cirrhosis, ulcerative colitis, dermatomyositis,
 CC polymyositis, scleroderma, mixed connective tissue disease and discoid
 CC lupus erythematosus. This sequence represents a human immunoregulator
 CC functional fragment peptide.

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 52; DB 22; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.022;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10

Db 4 VLPALPQVVC 13

RESULT 12

AAB71783

ID AAB71783 standard; peptide; 13 AA.

XX AC AAB71783;

XX XX 02-MAY-2001 (first entry)

XX DE Beta-human chorionic gonadotropin Satellin A1 branched peptide.

XX XX

KW Beta-human chorionic gonadotropin; beta-HCG; anti-HIV; cytostatic;
 KW antianemic; vascular; osteoporosis; antiinflammatory; gene therapy;
 KW maternin; MA peptide; pMA peptide; human immunodeficiency virus;
 KW HIV; cancer; wasting disorder; haematopoietic disorder; inflammation;
 KW angiogenic disorder.

XX Homo sapiens.

XX OS

XX PN WO200110907-A2.

XX PD 15-FEB-2001.

XX PF 05-AUG-2000; 2000WO-US21495.

XX XX 06-AUG-1999; 99US-0147825.

XX PR 13-MAR-2000; 2000US-0188777.

XX XX (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX PA Gallo R, Bryant J, Lunardi-Iskandar Y, Powell R, Reitz M;

XX PI Foulke J, Lewis G;

XX XX WPI; 2001-147510/15.

XX DR Cells that produce therapeutic beta-human chorionic gonadotropin

XX PT fragments, useful for the treatment of human immunodeficiency virus

XX PT infections, cancers, wasting disorders, hematopoietic disorders,

XX PT inflammation and angiogenic disorders -

XX PS Disclosure; Page 25; 185pp; English.

XX XX The present sequence is given in a specification relating to

XX CC therapeutic polypeptides originally isolated from human early pregnancy

XX CC urine, now synthetically produced, as well as functional equivalents of

XX CC these polypeptides. Novel beta-human chorionic gonadotropin (hCG)

XX CC fragments, designated Maternin (RTM) and referred to as MA and pMA

XX CC peptides, are disclosed. Both native and synthetic MA inhibited growth

XX CC of human tumour cells implanted into immuno-deficient mice by between 60

XX CC to 100%, relative to control studies. The therapeutic MA polypeptides

XX CC may be used for the prevention and treatment of a range of diseases and

XX CC disorders, including human immunodeficiency virus (HIV) infections,

XX CC cancers (especially Kaposi's sarcoma), wasting disorders, haematopoietic

XX CC disorders (e.g. anaemias, radiation mediated bone marrow damage and

XX CC trauma related blood loss), inflammation and angiogenic disorders.

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 52; DB 22; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.022;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10

Db 4 VLPALPQVVC 13

RESULT 13

AAU83032

ID AAU83032 standard; Peptide; 13 AA.

XX AC AAU83032;

XX XX 23-APR-2002 (first entry)

XX DE Human Satellin A1 (SAT_A1) peptide.

XX XX

XX KW Beta-human chorionic gonadotropin; beta-HCG; luteinising hormone; MA;

XX KW Maternin; human immunodeficiency virus; cancer; brain; breast; pancreas;

XX KW prostate; lung; kidney; haematopoietic malignancy; Kaposi's sarcoma; dog;

XX KW body cell mass; pathological angiogenesis; bacterial infection; anaemia;

XX KW chronic diarrhea; autoimmune disease; rheumatoid arthritis; diabetes;

XX KW chronic hepatitis; systemic lupus erythematosus; inflammation; cornea;

XX KW osteoporosis; parasitic infection; fungal infection; wound; burn; human;

XX KW horse; sheep; pig; cat; rat; Satellin; lutropin; HIV.

XX OS Homo sapiens.

XX XX WO200111048-A2.

XX PN

XX PD 15-FEB-2001.
 XX XX
 XX PF 05-AUG-2000; 2000WO-US21499.
 XX XX
 XX PR 06-AUG-1999; 99US-147825P.
 XX PR 13-MAR-2000; 2000US-18877P.
 XX XX
 XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 XX XX
 XX PI Gallo R, Bryant J, Lunardi-Iskandar Y;
 XX PI WPI; 2002-130122/17.
 XX DR
 XX XX
 XX PT New therapeutic MA polypeptides corresponding to human chorionic
 XX PT gonadotropin peptides, useful for treating and preventing cancers,
 XX PT pathological angiogenesis and loss of body cell mass -
 XX XX
 XX PS Disclosure; Page 4; 209pp; English.
 XX XX
 XX CC The invention relates to Maternin (MA) therapeutic polypeptides and other
 XX CC sequences derived from beta-human chorionic gonadotropin (beta-hCG) used
 XX CC for treating and/or preventing various medical conditions. The sequences
 XX CC are useful for inhibiting HIV replication and for the treatment and
 XX CC prevention of human immunodeficiency virus (HIV) infection, cancer (e.g.
 XX CC of the brain, breast, lung, pancreas, prostate or kidney), haematopoietic
 XX CC malignancy, preferably Kaposi's sarcoma, conditions characterised by loss
 XX CC of body cell mass, conditions associated with pathological angiogenesis,
 XX CC bacterial infections, chronic diarrhoea, anaemia, autoimmune disease,
 XX CC rheumatoid arthritis, diabetes, chronic hepatitis, systemic lupus
 XX CC erythematosus, wounds, burns, inflammation (especially of the cornea),
 XX CC osteoporosis, parasitic infections and fungal infections. Sequences
 XX CC AAU83014-AAU83063 represent therapeutic peptides and antigenic peptides
 XX CC of the invention.
 XX XX
 XX SQ Sequence 13 AA;
 XX
 Query Match 100.0%; Score 52; DB 23; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLPALPQVVC 10
 Db | | | | | | | | | |
 4 VLPALPQVVC 13
 RESULT 14
 AAW47489
 ID AAW47489 standard; Protein; 14 AA.
 XX AC AAW47489;
 XX XX
 XX DT 23-SEP-1998 (first entry)
 XX XX
 XX DE Human beta-hCG protein fragment (aa 45-58).
 XX XX
 XX KW Beta-human chorionic gonadotropin; beta-hCG; hematopoiesic cell;
 XX KW treatment; proliferation; human immunodeficiency virus; HIV; tumour;
 XX KW idiopathic thrombocytopenia purpura; anaemia; neutropenia;
 XX KW chemotherapy; radiation; autoimmune disease; genetic disorder.
 XX OS Homo sapiens.
 XX XX
 XX PN WO9749418-A1.
 XX XX
 XX PD 31-DEC-1997.
 XX XX
 XX PF 24-JUN-1997; 97WO-US11209.
 XX XX
 XX PR 09-SEP-1996; 96US-0709924.
 XX PR 24-JUN-1996; 96US-0669654.
 XX XX
 XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX PI Bryant J, Gallo RC, Lunardi-Iskandar Y;
 XX PI WPI; 1998-076906/07.
 XX XX
 XX PT Treating or preventing disease by increasing production of
 XX PT haematopoietic cells - using human chorionic gonadotropin or its
 XX PT fragments or derivatives, in vivo or in vitro, e.g. in cases of HIV
 XX PT infection, anaemia etc.
 XX XX
 XX PS Claim 7; Page 95; 162pp; English.
 XX XX
 XX CC AAW47474-W47508 represent fragments of the beta subunit of human
 XX CC chorionic gonadotropin which is used in a method for the treatment or
 XX CC prevention of disease, by increasing production of at least one type of
 XX CC haematopoietic cell. A method is also described in which non-terminally
 XX CC differentiated haematopoietic cells are treated in vitro to increase
 XX CC proliferation then returned to the patient. The method is specified for
 XX CC treating human immunodeficiency virus (HIV) infection, idiopathic
 XX CC thrombocytopenia purpura, anaemia or neutropenia, or subjects who have
 XX CC undergone chemotherapy or radiation treatment. More generally it can be
 XX CC used to treat a wide range of conditions involving haematopoietic
 XX CC failure, (non-) haematopoietic tumours, autoimmune disease and genetic
 XX CC disorders (using a transformed haematopoietic cell). The in vitro method
 XX CC can also be used to expand haematopoietic cells for subsequent
 XX CC therapeutic use.
 XX XX
 XX SQ Sequence 14 AA;
 XX
 Query Match 100.0%; Score 52; DB 19; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLPALPQVVC 10
 Db | | | | | | | | | |
 4 VLPALPQVVC 13
 RESULT 15
 AAW47497
 ID AAW47497 standard; Protein; 14 AA.
 XX AC AAW47497;
 XX XX
 XX DT 23-SEP-1998 (first entry)
 XX XX
 XX DE Human beta-hCG protein fragment (aa 44-57).
 XX XX
 XX KW Beta-human chorionic gonadotropin; beta-hCG; hematopoiesic cell; HIV;
 XX KW treatment; proliferation; human immunodeficiency virus; disulphide;
 XX KW idiopathic thrombocytopenia purpura; anaemia; neutropenia; tumour;
 XX KW chemotherapy; radiation; autoimmune disease; genetic disorder.
 XX OS Homo sapiens.
 XX XX
 XX FH Key Location/Qualifiers
 XX FT Disulfide-bond 1..14
 XX XX
 XX PN WO9749418-A1.
 XX XX
 XX PD 31-DEC-1997.
 XX XX
 XX PF 24-JUN-1997; 97WO-US11209.
 XX XX
 XX PR 09-SEP-1996; 96US-0709924.
 XX PR 24-JUN-1996; 96US-0669654.
 XX XX
 XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 XX XX
 XX PI Bryant J, Gallo RC, Lunardi-Iskandar Y;
 XX PI WPI; 1998-076906/07.
 XX XX

PT Treating or preventing disease by increasing production of
PT haematopoietic cells - using human chorionic gonadotropin or its
PT fragments or derivatives, in vivo or in vitro, e.g. in cases of HIV
PT infection, anaemia etc.
XX
PS Claim 7; Page 98; 162pp; English.
XX
XX AAW47474-W47508 represent fragments of the beta subunit of human
CC chorionic gonadotropin which is used in a method for the treatment or
CC prevention of disease, by increasing production of at least one type of
CC haematopoietic cell. A method is also described in which non-terminally
CC differentiated haematopoietic cells are treated in vitro to increase
CC proliferation then returned to the patient. The method is specified for
CC treating human immunodeficiency virus (HIV) infection, idiopathic
CC thrombocytopenia purpura, anaemia or neutropenia, or subjects who have
CC undergone chemotherapy or radiation treatment. More generally it can be
CC used to treat a wide range of conditions involving haematopoietic
CC failure, (non-) haematopoietic tumours, autoimmune disease and genetic
CC disorders (using a transformed haematopoietic cell). The in vitro method
CC can also be used to expand haematopoietic cells for subsequent
CC therapeutic use.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 52; DB 19; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
| | | | | | | |
Db 5 VLPALPQVVC 14

RESULT 16

AAW47483
ID AAW47483 standard; Protein; 14 AA.

XX AAW47483;

XX 23-SEP-1998 (first entry)

DE Human beta-hCG protein fragment (aa 44-57).

KW Beta-human chorionic gonadotropin; beta-hCG; hematopoiesic cell;
KW treatment; proliferation; human immunodeficiency virus; HIV; tumour;
KW idiopathic thrombocytopenia purpura; anaemia; neutropenia;
KW chemotherapy; radiation; autoimmune disease; genetic disorder.

XX Homo sapiens.

XX WO9749418-A1.

XX 31-DEC-1997.

XX 24-JUN-1997; 97WO-US11209.

XX 09-SEP-1996; 96US-0709924.

XX 24-JUN-1996; 96US-0669654.

XX (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX Bryant J, Gallo RC, Lunardi-Iskandar Y;

XX WPI; 1998-076906/07.

XX Treating or preventing disease by increasing production of
PT haematopoietic cells - using human chorionic gonadotropin or its
PT fragments or derivatives, in vivo or in vitro, e.g. in cases of HIV
PT infection, anaemia etc.

XX Claim 7; Page 94; 162pp; English.

XX AAW47474-W47508 represent fragments of the beta subunit of human

CC chorionic gonadotropin which is used in a method for the treatment or
CC prevention of disease, by increasing production of at least one type of
CC haematopoietic cell. A method is also described in which non-terminally
CC differentiated haematopoietic cells are treated in vitro to increase
CC proliferation then returned to the patient. The method is specified for
CC treating human immunodeficiency virus (HIV) infection, idiopathic
CC thrombocytopenia purpura, anaemia or neutropenia, or subjects who have
CC undergone chemotherapy or radiation treatment. More generally it can be
CC used to treat a wide range of conditions involving haematopoietic
CC failure, (non-) haematopoietic tumours, autoimmune disease and genetic
CC disorders (using a transformed haematopoietic cell). The in vitro method
CC can also be used to expand haematopoietic cells for subsequent
CC therapeutic use.

XX Sequence 14 AA;

Query Match 100.0%; Score 52; DB 19; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.024;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
| | | | | | | |
Db 5 VLPALPQVVC 14

RESULT 17

AAW50043

ID AAW50043 standard; peptide; 14 AA.

XX AAW50043;

XX 26-JUN-1998 (first entry)

XX Human chorionic gonadotropin beta-chain fragment.

KW Beta-chain; human; chorionic gonadotropin; beta-hCG; inhibition;
KW human immunodeficiency virus; HIV; infection; replication;
KW Kaposi's sarcoma; haematopoiesis.

XX Homo sapiens.

XX WO9749373-A2.

XX 31-DEC-1997.

XX 24-JUN-1997; 97WO-US11202.

XX 09-SEP-1996; 96US-0709948.

XX 24-JUN-1996; 96US-0669681.

XX (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX Bryant J, Gallo RC, Lunardi-Iskandar Y;

XX WPI; 1998-076887/07.

XX Human chorionic gonadotropin peptide derivatives - are active in
PT inhibiting, e.g. HIV infection or replication, Kaposi's Sarcoma or
PT have pro-haematopoietic activity

XX Claim 1; Page 105; 174pp; English.

XX The present sequence is a peptide derivative of the beta-chain of
CC human chorionic gonadotropin (beta-hCG). The peptide is active in
CC inhibiting, e.g. HIV infection or replication or Kaposi's sarcoma,
CC or has pro-haematopoietic activity.

XX Sequence 14 AA;

Query Match 100.0%; Score 52; DB 19; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.024;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
 Db 5 VLPALPQVVC 14

RESULT 18

AAW50092
 ID AAW50092 standard; peptide; 14 AA.

XX AC AAW50092;
 XX DT 26-JUN-1998 (first entry)
 XX DE Human chorionic gonadotropin beta-chain fragment.
 KW Beta-chain; human; chorionic gonadotropin; beta-hCG; treatment;
 KW prevention; wasting syndrome; viral infection; cancer;
 KW chronic cardiovascular disease; chemotherapy;
 KW radiation therapy.

OS Homo sapiens.

XX WO9749721-A1.

XX PD 31-DEC-1997.

XX PF 24-JUN-1997; 97WO-US11448.

XX PR 09-SEP-1996; 96US-0709933.

XX PR 24-JUN-1996; 96US-0669675.

XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX PI

XX PI Bryant J, Gallo RC, Lunardi-Iskandar Y;

XX DR WPI; 1998-077106/07.

XX PT Treating or preventing wasting syndrome - by administration of human
 PT chorionic gonadotropin, beta-hCG, peptides or derivatives of these

XX PS Example; Page 77; 126pp; English.

XX CC The present sequence is a peptide derivative of the beta-chain of
 CC human chorionic gonadotropin (beta-hCG). The peptide can be used
 CC to treat or prevent a wasting syndrome associated with viral
 CC infection, e.g. human immunodeficiency syndrome virus infection,
 CC cancer, chronic cardiovascular disease, chemotherapy or radiation
 CC therapy.

XX SQ Sequence 14 AA;

Query Match 100.0%; Score 52; DB 19; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.024;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
 Db 5 VLPALPQVVC 14

RESULT 19

AAW50084
 ID AAW50084 standard; peptide; 14 AA.

XX AC AAW50084;
 XX DT 26-JUN-1998 (first entry)
 XX DE Human chorionic gonadotropin beta-chain fragment.
 KW Beta-chain; human; chorionic gonadotropin; beta-hCG; treatment;
 KW prevention; wasting syndrome; viral infection; cancer;
 KW chronic cardiovascular disease; chemotherapy;

KW radiation therapy.

XX OS Homo sapiens.

XX PN WO9749721-A1.

XX PD 31-DEC-1997.

XX PF 24-JUN-1997; 97WO-US11448.

XX PR 09-SEP-1996; 96US-0709933.

XX PR 24-JUN-1996; 96US-0669675.

XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX PI

XX PI Bryant J, Gallo RC, Lunardi-Iskandar Y;

XX DR WPI; 1998-077106/07.

XX PT Treating or preventing wasting syndrome - by administration of human
 PT chorionic gonadotropin, beta-hCG, peptides or derivatives of these
 XX PS Claim 8; Page 74; 126pp; English.

XX CC The present sequence is a peptide derivative of the beta-chain of
 CC human chorionic gonadotropin (beta-hCG). The peptide can be used
 CC to treat or prevent a wasting syndrome associated with viral
 CC infection, e.g. human immunodeficiency syndrome virus infection,
 CC cancer, chronic cardiovascular disease, chemotherapy or radiation
 CC therapy.

XX SQ Sequence 14 AA;

Query Match 100.0%; Score 52; DB 19; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.024;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
 Db 4 VLPALPQVVC 13

RESULT 20

AAW50078

ID AAW50078 standard; peptide; 14 AA.

XX AC AAW50078;

XX DT 26-JUN-1998 (first entry)

XX DE Human chorionic gonadotropin beta-chain fragment.

XX KW Beta-chain; human; chorionic gonadotropin; beta-hCG; treatment;
 KW prevention; wasting syndrome; viral infection; cancer;
 KW chronic cardiovascular disease; chemotherapy;
 KW radiation therapy.

XX OS Homo sapiens.

XX PN WO9749721-A1.

XX PD 31-DEC-1997.

XX PF 24-JUN-1997; 97WO-US11448.

XX PR 09-SEP-1996; 96US-0709933.

XX PR 24-JUN-1996; 96US-0669675.

XX PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.

XX PI

XX PI Bryant J, Gallo RC, Lunardi-Iskandar Y;

XX DR WPI; 1998-077106/07.

```
XX Treating or preventing wasting syndrome - by administration of human
PT chorionic gonadotropin, beta-hCG, peptides or derivatives of these
XX
XX Claim 8; Page 73; 126pp; English.
XX
XX The present sequence is a peptide derivative of the beta-chain of
CC human chorionic gonadotropin (beta-hCG). The peptide can be used
CC to treat or prevent a wasting syndrome associated with viral
CC infection, e.g. human immunodeficiency syndrome virus infection,
CC cancer, chronic cardiovascular disease, chemotherapy or radiation
CC therapy.
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 52; DB 19; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLPALPQVVC 10
Db 5 VLPALPQVVC 14
|||||
RESULTS 21
AAW50049
ID AAW50049 standard; peptide; 14 AA.
XX
AC AAW50049;
XX
DT 26-JUN-1998 (first entry)
XX
DE Human chorionic gonadotropin beta-chain fragment.
XX
KW Beta-chain; human; chorionic gonadotropin; beta-hCG; inhibition;
KW human immunodeficiency virus; HIV; infection; replication;
KW Kaposi's sarcoma; haematopoiesis.
XX
OS Homo sapiens.
XX
PN WO9749373-A2.
XX
PD 31-DEC-1997.
XX
PF 24-JUN-1997; 97WO-US11202.
XX
PR 09-SEP-1996; 96US-0709948.
XX
PR 24-JUN-1996; 96US-0669681.
XX
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
PI Bryant J, Gallo RC, Lunardi-Iskandar Y;
XX
XX WPI; 1998-076887/07.
XX
XX Human chorionic gonadotropin peptide derivatives - are active in
PT inhibiting, e.g. HIV infection or replication, Kaposi's Sarcoma or
PT Kaposi's sarcoma; haematopoiesis.
XX
XX Homo sapiens.
XX
XX WO9749373-A2.
XX
PD 31-DEC-1997.
XX
PF 24-JUN-1997; 97WO-US11202.
XX
PR 09-SEP-1996; 96US-0709948.
XX
PR 24-JUN-1996; 96US-0669681.
XX
PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX
PI Bryant J, Gallo RC, Lunardi-Iskandar Y;
XX
XX WPI; 1998-076887/07.
XX
XX Human chorionic gonadotropin peptide derivatives - are active in
PT inhibiting, e.g. HIV infection or replication, Kaposi's Sarcoma or
PT have pro-haematopoietic activity
XX
XX Claim 1; Page 106; 174pp; English.
XX
XX The present sequence is a peptide derivative of the beta-chain of
CC human chorionic gonadotropin (beta-hCG). The peptide is active in
CC inhibiting, e.g. HIV infection or replication or Kaposi's sarcoma,
CC or has pro-haematopoietic activity.
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 52; DB 19; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLPALPQVVC 10
Db 5 VLPALPQVVC 14
|||||
RESULTS 23
AAB71784
ID AAB71784 standard; peptide; 14 AA.
XX
AC AAB71784;
XX
DT 02-MAY-2001 (first entry)
XX
DE Beta-human chorionic gonadotropin Satellin A2 circularised peptide.
XX
KW Beta-human chorionic gonadotropin; beta-hCG; anti-HIV; cytostatic;
KW antianemic; vascular; osteopathic; antiinflammatory; gene therapy;
KW maternin; MA peptide; pMA peptide; human immunodeficiency virus;
KW HIV; cancer; wasting disorder; haematopoietic disorder; inflammation;
KW angiogenic disorder; cyclic; circular.
XX
XX Sequence 14 AA;
SQ
Query Match 100.0%; Score 52; DB 19; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLPALPQVVC 10
Db 5 VLPALPQVVC 14
|||||
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OS Homo sapiens.
 XX WO200110907-A2.
 XX 15-FEB-2001.
 XX 05-AUG-2000; 2000WO-US21495.
 XX 06-AUG-1999; 99US-0147825.
 PR 13-MAR-2000; 2000US-0188777.
 XX (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 XX Gallo R, Bryant J, Lunardi-Iskandar Y, Powell R, Reitz M;
 PI Foulke J, Lewis G;
 XX WPI; 2001-147510/15.
 XX Cells that produce therapeutic beta-human chorionic gonadotropin
 PT fragments, useful for the treatment of human immunodeficiency virus
 PT infections, cancers, wasting disorders, hematopoietic disorders,
 PT inflammation and angiogenic disorders -
 XX Example; Page 121; 185pp; English.
 XX The present sequence is given in a specification relating to
 CC therapeutic polypeptides originally isolated from human early pregnancy
 CC urine, now synthetically produced, as well as functional equivalents of
 CC these polypeptides. Novel beta-human chorionic gonadotropin (hCG)
 CC fragments, designated Maternin (RTM) and referred to as MA and pMA
 CC peptides, are disclosed. Both native and synthetic MA inhibited growth
 CC of human tumour cells implanted into immuno-deficient mice by between 60
 CC to 100%, relative to control studies. The therapeutic MA polypeptides
 CC may be used for the prevention and treatment of a range of diseases and
 CC disorders, including human immunodeficiency virus (HIV) infections,
 CC cancers (especially Kaposi's sarcoma), wasting disorders, haematopoietic
 CC disorders (e.g. anaemias, radiation mediated bone marrow damage and
 CC trauma related blood loss), inflammation and angiogenic disorders.
 XX SQ Sequence 14 AA;
 Query Match 100.0%; Score 52; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLPALPQVVC 10
 DB 5 VLPALPQVVC 14
 |||||
 RESULT 24
 ID AAB71804 standard; peptide; 14 AA.
 XX AAB71804;
 XX 02-MAY-2001 (first entry)
 XX Beta-hCG Satelin A2 sequence active peptide.
 XX Human; beta-human chorionic gonadotropin; beta-hCG; satelin A2;
 KW anti-HIV; cytostatic; antianemic; vascular; osteopathic;
 KW antiinflammatory; gene therapy; maternin; MA peptide; pMA peptide;
 KW human immunodeficiency virus; HIV; cancer; wasting disorder;
 KW haematopoietic disorder; inflammation; angiogenic disorder.
 XX Homo sapiens.
 OS WO200110907-A2.
 XX 15-FEB-2001.
 XX 05-AUG-2000; 2000WO-US21495.
 XX (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 XX Gallo R, Bryant J, Lunardi-Iskandar Y, Powell R, Reitz M;
 PI Foulke J, Lewis G;
 XX WPI; 2001-147510/15.
 XX Cells that produce therapeutic beta-human chorionic gonadotropin
 PT fragments, useful for the treatment of human immunodeficiency virus
 PT infections, cancers, wasting disorders, hematopoietic disorders,
 PT inflammation and angiogenic disorders -
 XX Example; Page 25; 185pp; English.
 XX The present sequence is given in a specification relating to
 CC therapeutic polypeptides originally isolated from human early pregnancy
 CC urine, now synthetically produced, as well as functional equivalents of
 CC these polypeptides. Novel beta-human chorionic gonadotropin (hCG)
 CC fragments, designated Maternin (RTM) and referred to as MA and pMA
 CC peptides, are disclosed. Both native and synthetic MA inhibited growth
 CC of human tumour cells implanted into immuno-deficient mice by between 60
 CC to 100%, relative to control studies. The therapeutic MA polypeptides
 CC may be used for the prevention and treatment of a range of diseases and
 CC disorders, including human immunodeficiency virus (HIV) infections,
 CC cancers (especially Kaposi's sarcoma), wasting disorders, haematopoietic
 CC disorders (e.g. anaemias, radiation mediated bone marrow damage and
 CC trauma related blood loss), inflammation and angiogenic disorders.
 XX SQ Sequence 14 AA;
 Query Match 100.0%; Score 52; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLPALPQVVC 10
 DB 5 VLPALPQVVC 14
 |||||
 RESULT 25
 ID AAU83033 standard; Peptide; 14 AA.
 XX AAU83033;
 XX 23-APR-2002 (first entry)
 XX Human Satelin A2 (SAT_A2) peptide.
 XX Beta-human chorionic gonadotropin; beta-hCG; luteinising hormone; MA;
 KW Maternin; human immunodeficiency virus; cancer; brain; breast; pancreas;
 KW prostate; lung; kidney; haematopoietic malignancy; Kaposi's sarcoma; dog;
 KW body cell mass; pathological angiogenesis; bacterial infection; anaemia;
 KW chronic diarrhoea; autoimmune disease; rheumatoid arthritis; diabetes;
 KW chronic hepatitis; systemic lupus erythematosus; inflammation; cornea;
 KW osteoporosis; parasitic infection; fungal infection; wound; burn; human;
 KW horse; sheep; pig; cat; rat; Satelin; lutropin; HIV.
 XX Homo sapiens.
 OS WO200111048-A2.
 XX 15-FEB-2001.
 XX 05-AUG-2000; 2000WO-US21499.
 XX 06-AUG-1999; 99US-147825P.
 PR 13-MAR-2000; 2000US-188777P.

Wed Dec 4 11:39:39 2002

PA (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
 XX
 PI Gallo R, Bryant J, Lunardi-Iskandar Y;
 XX
 XX WPI; 2002-130122/17.
 XX
 DR New therapeutic MA polypeptides corresponding to human chorionic
 PT gonadotropin peptides, useful for treating and preventing cancers,
 PT pathological angiogenesis and loss of body cell mass -
 XX
 XX Examples; Page 121; 209pp; English.
 PS
 XX
 XX The invention relates to Maternin (MA) therapeutic polypeptides and other
 CC sequences derived from beta-human chorionic gonadotropin (beta-hCG) used
 CC for treating and/or preventing various medical conditions. The sequences
 CC are useful for inhibiting HIV replication and for the treatment and
 CC prevention of human immunodeficiency virus (HIV) infection, cancer (e.g.
 CC of the brain, breast, lung, pancreas, prostate or kidney), haematopoietic
 CC malignancy, preferably Kaposi's sarcoma, conditions characterised by loss
 CC of body cell mass, conditions associated with pathological angiogenesis,
 CC bacterial infections, chronic diarrhoea, anaemia, autoimmune disease,
 CC rheumatoid arthritis, diabetes, chronic hepatitis, systemic lupus
 CC erythematosus, wounds, burns, inflammation (especially of the cornea),
 CC osteoporosis, parasitic infections and fungal infections. Sequences
 CC AAU83014-AAU83063 represent therapeutic peptides and antigenic peptides
 CC of the invention.
 XX
 SQ Sequence 14 AA;
 Query Match 100.0%; Score 52; DB 23; Length 14;
 Best Local Similarity 100.0%; Pred. NO. 0.024;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLPALPQVVC 10
 DB 5 VLPALPQVVC 14
 Search completed: December 4, 2002, 11:26:06
 Job time : 23.25 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 11:24:35 ; Search time 8.5 seconds
(without alignments)
34.615 Million cell updates/sec

Title: US-09-821-380-3

Perfect score: 52

Sequence: 1 VLPALPQVVC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	12	2	US-08-709-924-22
2	52	100.0	12	2	Sequence 22, Appl
3	52	100.0	12	2	Sequence 22, Appl
4	52	100.0	13	4	US-08-709-948-22
5	52	100.0	13	2	US-08-709-924-6
6	52	100.0	13	4	US-08-709-925-6
7	52	100.0	14	2	US-08-709-948-6
8	52	100.0	14	2	US-08-709-924-12
9	52	100.0	14	2	US-08-709-924-18
10	52	100.0	14	2	US-08-709-924-26
11	52	100.0	14	2	US-08-709-925-12
12	52	100.0	14	2	US-08-709-925-18
13	52	100.0	14	2	US-08-709-925-26
14	52	100.0	14	4	US-08-709-948-12
15	52	100.0	14	4	US-08-709-948-18
16	52	100.0	14	4	US-08-709-948-26
17	52	100.0	93	4	US-08-918-288-70
18	52	100.0	98	2	US-08-709-924-23
19	52	100.0	98	2	US-08-709-925-23
20	52	100.0	98	4	US-08-709-948-23
21	52	100.0	114	1	US-08-425-673-7
22	52	100.0	114	1	US-08-425-673-8
23	52	100.0	114	1	US-08-425-673-9
24	52	100.0	114	4	US-08-918-288-69
25	52	100.0	114	4	US-08-282-357-69
26	52	100.0	117	1	US-08-425-673-11
27	52	100.0	117	1	US-08-425-673-12

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Sequence 2, Appl
Sequence 10, Appl
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Sequence 10, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 11, Appl
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Sequence 16, Appl
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Sequence 36, Appl
Sequence 21, Appl
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Sequence 6, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 18, Appl
Sequence 3, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 4, Appl
Sequence 8, Appl

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1 US-09-282-357-15
1 US-09-282-357-18
1 US-08-918-288-3
1 US-08-918-288-39
1 US-09-282-357-3
1 US-09-282-357-39
1 US-08-804-166-4
1 US-08-910-991-4
1 US-08-804-166-8

ALIGNMENTS

RESULT 1

US-08-709-924-22
; Sequence 22, Application US/08709924
; Patent No. 5968513
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHODS OF PROMOTING HEMATOPOIESIS
; TITLE OF INVENTION: USING DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,924
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 8769-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-709-924-22

Query Match 100.0%; Score 52; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
Db 2 VLPALPQVVC 11

RESULT 2

US-08-709-925-22
Sequence 22, Application US/08709925
Patent No. 5997871

GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
APPLICANT: Bryant, Joseph
APPLICANT: Lunardi-Iskandar, Yanto
TITLE OF INVENTION: TREATMENT AND PREVENTION OF CANCER BY
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 8769-016
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,925
FILING DATE: 09-SEP-1996
CLASSIFICATION: 512

ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8769-017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-709-925-22

Query Match 100.0%; Score 52; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
Db 2 VLPALPQVVC 11

RESULT 3

US-08-709-948-22
Sequence 22, Application US/08709948
Patent No. 6319504

GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
APPLICANT: Bryant, Joseph
APPLICANT: Lunardi-Iskandar, Yanto
TITLE OF INVENTION: TREATMENT AND PREVENTION OF HIV INFECTION
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 8769-016
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,948
FILING DATE: 09-SEP-1996
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8769-016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-709-948-22

Query Match 100.0%; Score 52; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
Db 2 VLPALPQVVC 11

RESULT 4

US-08-709-924-6
Sequence 6, Application US/08709924
Patent No. 5968513

GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
APPLICANT: Bryant, Joseph
APPLICANT: Lunardi-Iskandar, Yanto
TITLE OF INVENTION: METHODS OF PROMOTING HEMATOPOIESIS
TELECOMMUNICATION INFORMATION:
REFERENCE/DOCKET NUMBER: 8769-017
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM: disk
US-08-709-924-6

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,924
FILING DATE: 09-SEP-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8769-018
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-709-924-6

Query Match 100.0%; Score 52; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 4 VLPALPQVVC 13

RESULT 5
US-08-709-925-6
Sequence 6, Application US/08709925
Patent No. 5937871
GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
APPLICANT: Bryant, Joseph
APPLICANT: Lunardi-Iskandar, Yanto
TITLE OF INVENTION: TREATMENT AND PREVENTION OF CANCER BY
TITLE OF INVENTION: ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,925
FILING DATE: 09-SEP-1996
CLASSIFICATION: 512
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8769-017
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-709-925-6

Query Match 100.0%; Score 52; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 4 VLPALPQVVC 13

RESULT 6
US-08-709-948-6
Sequence 6, Application US/08709948
Patent No. 6319504
GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
APPLICANT: Bryant, Joseph
APPLICANT: Lunardi-Iskandar, Yanto
TITLE OF INVENTION: TREATMENT AND PREVENTION OF HIV INFECTION
TITLE OF INVENTION: BY ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,948
FILING DATE: 09-SEP-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8769-016
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-709-948-6

Query Match 100.0%; Score 52; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 4 VLPALPQVVC 13

RESULT 7
US-08-709-924-12
Sequence 12, Application US/08709924
Patent No. 5968513
GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
APPLICANT: Bryant, Joseph
APPLICANT: Lunardi-Iskandar, Yanto
TITLE OF INVENTION: METHODS OF PROMOTING HEMATOPOIESIS
TITLE OF INVENTION: USING DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-709-924-18

Query Match 100.0%; Score 52; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 4 VLPALPQVVC 13

RESULT 9
US-08-709-924-26
; Sequence 26, Application US/08709924
; Patent No. 5968513
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHODS OF PROMOTING HEMATOPOIESIS
; TITLE OF INVENTION: USING DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,924
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-08-709-924-26

Query Match 100.0%; Score 52; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 5 VLPALPQVVC 14

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RESULT 10
US-08-709-925-12
; Sequence 12, Application US/08709925
; Patent No. 5997871
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF CANCER BY
; TITLE OF INVENTION: ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,925
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 512
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-709-925-12

Query Match 100.0%; Score 52; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
| | | | | | | |
Db 5 VLPALPQVVC 14

RESULT 11
US-08-709-925-18
; Sequence 18, Application US/08709925
; Patent No. 5997871
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF CANCER BY
; TITLE OF INVENTION: ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,925
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 512
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-709-925-18

Query Match 100.0%; Score 52; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
| | | | | | | |
Db 4 VLPALPQVVC 13

RESULT 12
US-08-709-925-26
; Sequence 26, Application US/08709925
; Patent No. 5997871
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF CANCER BY
; TITLE OF INVENTION: ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,925
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 512
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
; MOLECULE TYPE: peptide
US-08-709-925-26

Query Match 100.0%; Score 52; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
| | | | | | | |
Db 5 VLPALPQVVC 14

RESULT 13

US-08-709-948-12
; Sequence 12, Application US/08709948
; Patent No. 6319504
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HIV INFECTION
; TITLE OF INVENTION: BY ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROPHIN
; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 09-SEP-1996
APPLICATION NUMBER: US/087709,948
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8769-016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-709-948-12

Query Match 100.0%; Score 52; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
| | | | | | | |
Db 5 VLPALPQVVC 14

RESULT 14

US-08-709-948-18
; Sequence 18, Application US/08709948
; Patent No. 6319504
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HIV INFECTION
; TITLE OF INVENTION: BY ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROPHIN
; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/087709,948
FILING DATE: 09-SEP-1996
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8769-016
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-709-948-18

Query Match 100.0%; Score 52; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
| | | | | | | |
Db 4 VLPALPQVVC 13

RESULT 15

US-08-709-948-26
; Sequence 26, Application US/08709948
; Patent No. 6319504
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HIV INFECTION
; TITLE OF INVENTION: BY ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROPHIN
; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/087709,948
FILING DATE: 09-SEP-1996
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8769-016
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
US-08-709-948-26

Query Match 100.0%; Score 52; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 5 VLPALPQVVC 14

RESULT 16

US-08-918-288-70
; Sequence 70, Application US/08918288
; Patent No. 6238890
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,288
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/282,357
FILING DATE:
APPLICATION NUMBER: 08/853,524
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 08/199,382
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29500-20050.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-887-0763
TELEX:

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-918-288-70

Query Match 100.0%; Score 52; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 48 VLPALPQVVC 57

RESULT 17

US-09-282-357-70
; Sequence 70, Application US/09282357
; Patent No. 6242580
; GENERAL INFORMATION:
; APPLICANT: BOIME, Irving
; APPLICANT: MOYLE, William R.
; TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
; TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,357
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/918,288
FILING DATE: 25 AUG-1997
APPLICATION NUMBER: 08/853,524
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 08/199,382
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29500-20050.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-887-0763
TELEX:

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-282-357-70

Query Match 100.0%; Score 52; DB 4; Length 93;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 48 VLPALPQVVC 57

RESULT 18

US-08-709-924-23
; Sequence 23, Application US/08709924
; Patent No. 5968513
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHODS OF PROMOTING HEMATOPOIESIS
; USING DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN

```

; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/709,924
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-709-924-23

Query Match 100.0%; Score 52; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
DB 1 VLPALPQVVC 10

RESULT 19
US-08-709-925-23
; Sequence 23, Application US/08709925
; Patent No. 5997871
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF CANCER BY
; TITLE OF INVENTION: ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 512
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-017

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-709-925-23

Query Match 100.0%; Score 52; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
DB 1 VLPALPQVVC 10

RESULT 20
US-08-709-948-23
; Sequence 23, Application US/08709948
; Patent No. 6319504
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HIV INFECTION
; TITLE OF INVENTION: BY ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONADOT
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,948
; FILING DATE: 09-SEP-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-709-948-23

Query Match 100.0%; Score 52; DB 4; Length 98;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
DB 1 VLPALPQVVC 10

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RESULT 21
US-08-425-673-7
; Sequence 7, Application US/08425673
; Patent No. 5508261
; GENERAL INFORMATION:
; APPLICANT: Moyle, William R.
; APPLICANT: Campbell, Robert K.
; TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
; TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
; TITLE OF INVENTION: Methods For Preparing and Using Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: P.O. Box 1267
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08551
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,673
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/717,151
; FILING DATE: 18-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Muccino, Richard R.
; REGISTRATION NUMBER: 32,538
; REFERENCE/DOCKET NUMBER: UMD 1.0-004
; TELEPHONE: (609) 466-3407
; TELEFAX: (609) 466-2760
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-425-673-7

Query Match 100.0%; Score 52; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 48 VLPALPQVVC 57

RESULT 22
US-08-425-673-8
; Sequence 8, Application US/08425673
; Patent No. 5508261
; GENERAL INFORMATION:
; APPLICANT: Moyle, William R.
; APPLICANT: Campbell, Robert K.
; TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
; TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
; TITLE OF INVENTION: Methods For Preparing and Using Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: P.O. Box 1267
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: USA

Query Match 100.0%; Score 52; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 48 VLPALPQVVC 57

RESULT 23
US-08-425-673-9
; Sequence 9, Application US/08425673
; Patent No. 5508261
; GENERAL INFORMATION:
; APPLICANT: Moyle, William R.
; APPLICANT: Campbell, Robert K.
; TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
; TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
; TITLE OF INVENTION: Methods For Preparing and Using Same
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard R. Muccino
; STREET: P.O. Box 1267
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08551
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/425,673
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/717,151
; FILING DATE: 18-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Muccino, Richard R.
; REGISTRATION NUMBER: 32,538
; REFERENCE/DOCKET NUMBER: UMD 1.0-004
; TELEPHONE: (609) 466-3407
; TELEFAX: (609) 466-2760
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 114 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-425-673-8

Query Match 100.0%; Score 52; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 48 VLPALPQVVC 57
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 466-3407
TELEFAX: (609) 466-2760
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-425-673-9

Query Match 100.0%; Score 52; DB 1; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 48 VLPALPQVVC 57

RESULT 24
US-08-918-288-69
Sequence 69, Application US/08918288
Patent No. 6238890
GENERAL INFORMATION:
APPLICANT: BOIME, Irving
TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918.288
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/282,357
FILING DATE:
APPLICATION NUMBER: 08/853,524
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 08/199,382
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29500-20050.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-887-0763
TELEX:

INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-918-288-69

Query Match 100.0%; Score 52; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.047;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLPALPQVVC 10
Db 48 VLPALPQVVC 57

RESULT 25
US-09-282-357-69
Sequence 69, Application US/09282357
Patent No. 6242580
GENERAL INFORMATION:
APPLICANT: BOIME, Irving
APPLICANT: MOYLE, William R.
TITLE OF INVENTION: SINGLE-CHAIN FORMS OF THE
TITLE OF INVENTION: GLYCOPROTEIN HORMONE QUARTET
NUMBER OF SEQUENCES: 83
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Avenue, NW, suite 5500
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,357
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/918,288
FILING DATE: 25 AUG-1997
APPLICATION NUMBER: 08/853,524
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: 08/199,382
FILING DATE: 18-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29500-20050.25
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
TELEFAX: 202-887-0763
TELEX:

INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-282-357-69

Query Match 100.0%; Score 52; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 0.047;
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QY 1 VLPALPQVVC 10
Db 48 VLPALPQVVC 57

Search completed: December 4, 2002, 11:29:14
Job time : 8.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:27:25 ; Search time 5 Seconds
(without alignments)
32.485 Million cell updates/sec

Title: US-09-821-380-3

Perfect score: 52

Sequence: 1 VLPALPQVVC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 103943 seqs, 16242309 residues

Total number of hits satisfying chosen parameters: 103943

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database : Published Applications AA:*

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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	52	100.0	13	US-09-821-380-2	Sequence 2, Appl
3	52	100.0	17	US-09-821-380-1	Sequence 1, Appl
4	52	100.0	20	US-09-915-676-9	Sequence 9, Appl
5	52	100.0	20	US-09-466-320-6	Sequence 6, Appl
6	52	100.0	141	US-09-813-398-3	Sequence 3, Appl
7	52	100.0	165	US-09-915-676-1	Sequence 1, Appl
8	52	100.0	165	US-09-466-320-14	Sequence 14, Appl
9	52	100.0	195	US-09-780-933-30	Sequence 30, Appl
10	52	100.0	196	US-09-780-933-29	Sequence 29, Appl
11	52	100.0	307	US-09-756-186-4	Sequence 4, Appl
12	52	100.0	336	US-09-756-186-8	Sequence 8, Appl
13	47	90.4	122	US-09-813-398-4	Sequence 4, Appl
14	40	76.9	113	US-09-730-617-44	Sequence 44, Appl
15	37	71.2	99	US-09-730-617-41	Sequence 41, Appl
16	37	71.2	141	US-09-730-617-47	Sequence 47, Appl
17	37	71.2	141	US-09-730-617-48	Sequence 48, Appl
18	37	71.2	654	US-09-969-528-10	Sequence 10, Appl
19	35	67.3	7	US-09-821-380-9	Sequence 9, Appl

20	67.3	35	8	10	US-09-821-380-10	Sequence 10, Appl
21	67.3	35	10	10	US-09-821-380-4	Sequence 4, Appl
22	65.4	34	67	10	US-09-864-761-44768	Sequence 44768, A
23	65.4	34	85	10	US-09-864-761-36293	Sequence 36293, A
24	65.4	34	350	9	US-09-361-655-14	Sequence 14, Appl
25	63.5	33	128	10	US-09-864-761-36308	Sequence 36308, A
26	63.5	33	162	10	US-09-864-761-43620	Sequence 43620, A
27	63.5	33	214	10	US-09-995-515-5	Sequence 5, Appl
28	63.5	33	364	9	US-10-066-500-65	Sequence 65, Appl
29	63.5	33	364	12	US-10-117-178-2	Sequence 2, Appl
30	63.5	33	2472	10	US-09-815-242-5064	Sequence 5064, Ap
31	61.5	32	54	10	US-09-938-719-11	Sequence 11, Appl
32	61.5	32	54	10	US-09-938-719-11	Sequence 11, Appl
33	61.5	32	54	10	US-09-938-703-11	Sequence 11, Appl
34	61.5	32	59	10	US-09-867-550-1796	Sequence 1796, Ap
35	61.5	32	91	10	US-09-864-761-43325	Sequence 43325, A
36	61.5	32	96	10	US-09-764-870-454	Sequence 454, App
37	61.5	32	131	10	US-09-764-870-293	Sequence 293, App
38	61.5	32	182	10	US-09-764-870-293	Sequence 293, App
39	61.5	32	291	10	US-09-764-864-1293	Sequence 1293, Ap
40	61.5	32	40	10	US-09-725-285-2	Sequence 2, Appl
41	61.5	32	352	10	US-09-759-841-2	Sequence 2, Appl
42	61.5	32	352	10	US-09-779-879A-2	Sequence 2, Appl
43	61.5	32	352	10	US-09-779-879A-22	Sequence 22, Appl
44	61.5	32	352	10	US-09-779-880A-2	Sequence 22, Appl
45	61.5	32	352	10	US-09-779-880A-22	Sequence 22, Appl
46	61.5	32	352	10	US-09-813-653-15	Sequence 15, Appl
47	61.5	32	352	10	US-09-813-653-17	Sequence 17, Appl
48	61.5	32	352	10	US-09-796-202-1	Sequence 1, Appl
49	61.5	32	352	10	US-09-195-662A-2	Sequence 2, Appl
50	61.5	32	352	10	US-09-339-912A-2	Sequence 2, Appl
51	61.5	32	352	10	US-09-938-719-5	Sequence 5, Appl
52	61.5	32	352	10	US-09-939-226-5	Sequence 5, Appl
53	61.5	32	352	10	US-09-938-703-5	Sequence 5, Appl
54	61.5	32	352	10	US-09-502-783A-2	Sequence 2, Appl
55	61.5	32	352	12	US-10-106-623-2	Sequence 2, Appl
56	61.5	32	352	12	US-10-106-623-20	Sequence 20, Appl
57	61.5	32	398	10	US-09-925-301-1264	Sequence 1264, Ap
58	61.5	32	414	10	US-09-820-893-69	Sequence 69, Appl
59	61.5	32	438	10	US-09-815-242-12025	Sequence 12025, A
60	61.5	32	438	10	US-09-894-993-2	Sequence 2, Appl
61	61.5	32	457	10	US-09-888-615-110	Sequence 110, App
62	61.5	32	480	10	US-09-820-893-108	Sequence 108, App
63	61.5	32	653	10	US-09-746-801A-13	Sequence 13, Appl
64	61.5	32	684	10	US-09-815-242-10712	Sequence 10712, A
65	61.5	32	986	9	US-09-870-759-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1

US-09-821-380-3
; Sequence 3, Application US/09821380
; Patent No. US20020064501A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Ahmed
; APPLICANT: Benner, Robert
; APPLICANT: Savelkoul, Josef
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-47990S
; CURRENT APPLICATION NUMBER: US/09/821, 380
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/NL99/00313
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/777,777
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: EP 98201695.8
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent version 3.0

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; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fragment of peptide immunoregulator
US-09-821-380-3

Query Match      100.0%; Score 52; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
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Db 1 VLPALPQVVC 10

RESULT 2
US-09-821-380-2
; Sequence 2, Application US/09821380
; Patent No. US20020064501A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Ahmed
; APPLICANT: Benner, Robert
; APPLICANT: Savelkoul, Josef
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-4799US
; CURRENT APPLICATION NUMBER: US/09/821,380
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/NL99/00313
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/???,???
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: EP 98201695.8
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fragment of peptide immunoregulator
US-09-821-380-2

Query Match      100.0%; Score 52; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 VLPALPQVVC 13

RESULT 3
US-09-821-380-1
; Sequence 1, Application US/09821380
; Patent No. US20020064501A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Ahmed
; APPLICANT: Benner, Robert
; APPLICANT: Savelkoul, Josef
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-4799US
; CURRENT APPLICATION NUMBER: US/09/821,380
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/NL99/00313
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/???,???
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: EP 98201695.8
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; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Peptide immunoregulator
US-09-821-380-1

Query Match      100.0%; Score 52; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 VLPALPQVVC 17

RESULT 4
US-09-915-676-9
; Sequence 9, Application US/09915676
; Patent No. US20020164338A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Combined Approach to Treatment of Cancer
; FILE REFERENCE: 50450-8027.US01
; CURRENT APPLICATION NUMBER: US/09/915,676
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 09/571,497
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/134,419
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/134,432
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-676-9

Query Match      100.0%; Score 52; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
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Db 11 VLPALPQVVC 20

RESULT 5
US-09-466-320-6
; Sequence 6, Application US/09466320
; Patent No. US2002025939A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick
; TITLE OF INVENTION: Chorionic Gonadotropin DNA Vaccines and
; FILE REFERENCE: 0450-0026.30
; CURRENT APPLICATION NUMBER: US/09/466,320
; CURRENT FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: US 60/112,910
; PRIOR FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
```

```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide
US-09-466-320-6

Query Match      100.0%; Score 52; DB 10; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0031;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 11 VLPALPQVVC 20

RESULT 6
US-09-813-398-3
; Sequence 3, Application US/09813398
; Patent No. US20020169292A1
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
; APPLICANT: Mariusz W. Szkudlinski
; APPLICANT: University of Maryland
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
; FILE REFERENCE: UOFMD.003C1
; CURRENT APPLICATION NUMBER: US/09/813,398
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/05908
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/19772
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-09-813-398-3

Query Match      100.0%; Score 52; DB 9; Length 141;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 49 VLPALPQVVC 58

RESULT 7
US-09-915-676-1
; Sequence 1, Application US/09915676
; Patent No. US20020164338A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick L.
; TITLE OF INVENTION: Combined Approach to Treatment of Cancer
; TITLE OF INVENTION: with hcg vaccines
; FILE REFERENCE: 50450-8027.US01
; CURRENT APPLICATION NUMBER: US/09/915,676
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US/09/571,497
; PRIOR FILING DATE: 2000-05-15
; PRIOR APPLICATION NUMBER: US 60/134,419
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/134,432
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-676-1

Query Match      100.0%; Score 52; DB 9; Length 165;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 68 VLPALPQVVC 77

RESULT 8
US-09-466-320-14
; Sequence 14, Application US/09466320
; Patent No. US20020025939A1
; GENERAL INFORMATION:
; APPLICANT: Iversen, Patrick
; TITLE OF INVENTION: Chorionic Gonadotropin DNA Vaccines and
; TITLE OF INVENTION: Methods
; FILE REFERENCE: 0450-0026.30
; CURRENT APPLICATION NUMBER: US/09/466,320
; CURRENT FILING DATE: 1999-12-17
; EARLIER APPLICATION NUMBER: US 60/112,910
; EARLIER FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hcg beta sub unit
US-09-466-320-14

Query Match      100.0%; Score 52; DB 10; Length 165;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 68 VLPALPQVVC 77

RESULT 9
US-09-780-933-30
; Sequence 30, Application US/09780933
; Patent No. US20020127652A1
; GENERAL INFORMATION:
; APPLICANT: SCHAMBYE, HANS T.
; APPLICANT: ANDERSEN, KIM V.
; APPLICANT: VAN DEN HAZEL, BART
; APPLICANT: CHRISTIANSEN, JESPER
; APPLICANT: JEPPESEN, CLAUD B.
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
; FILE REFERENCE: 31-00100005
; CURRENT APPLICATION NUMBER: US/09/780,933
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PA 2000 00220
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,035
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PA 2000 01092
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,558
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-933-30

Query Match      100.0%; Score 52; DB 10; Length 195;
Best Local Similarity 100.0%; Pred. No. 0.031;
```

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
| | | | | | | |
Db 132 VLPALPQVVC 141

RESULT 10

US-09-780-933-29
; Sequence 29, Application US/09780933
; Patent No. US20020127652A1
; GENERAL INFORMATION:
; APPLICANT: SCHAMBYE, HANS T.
; APPLICANT: ANDERSEN, KIM V.
; APPLICANT: VAN DEN HAZEL, BART
; APPLICANT: CHRISTIANSEN, JESPER
; APPLICANT: JEPPESEN, CLAUS B.
; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONES
; FILE REFERENCE: 31-001000US
; CURRENT APPLICATION NUMBER: US/09/780,933
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PA 2000 00220
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 60/184,035
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: PA 2000 01092
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,558
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 196
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-780-933-29

Query Match 100.0%; Score 52; DB 10; Length 196;

Best Local Similarity 100.0%; Pred. No. 0.032;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
| | | | | | | |
Db 133 VLPALPQVVC 142

RESULT 11

US-09-756-186-4
; Sequence 4, Application US/09756186
; Patent No. US20010014333A1
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/804,166
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: CAMPBELL-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-756-186-4

Query Match 100.0%; Score 52; DB 10; Length 307;

Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
| | | | | | | |
Db 210 VLPALPQVVC 219

RESULT 12

US-09-756-186-8
; Sequence 8, Application US/09756186
; Patent No. US20010014333A1
; GENERAL INFORMATION:
; APPLICANT: Campbell, Robert K.
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Chappel, Scott C.
; TITLE OF INVENTION: HYBRID PROTEINS
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 22207
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/756,186
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/804,166
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: CAMPBELL-2A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-756-186-8

Query Match

100.0%; Score 52; DB 10; Length 336;

Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
||| |||||
Db 239 VLPALPQVVC 248

RESULT 13

US-09-813-398-4
; Sequence 4, Application US/09813398
; Patent No. US20020169292A1
; GENERAL INFORMATION:
; APPLICANT: Bruce D. Weintraub
; APPLICANT: Mariusz W. Szkudlinski
; APPLICANT: University of Maryland
; TITLE OF INVENTION: CYSTINE KNOT GROWTH FACTOR MUTANTS
; FILE REFERENCE: UOPWD.003C1
; CURRENT APPLICATION NUMBER: US/09/813.398
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: PCT/US99/05908
; PRIOR FILING DATE: 1999-03-19
; PRIOR APPLICATION NUMBER: PCT/US98/19772
; PRIOR FILING DATE: 1998-09-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 122
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
US-09-813-398-4

Query Match 90.4%; Score 47; DB 9; Length 122;
Best Local Similarity 90.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
||| |||||
Db 49 VLPPLPQVVC 58

RESULT 14

US-09-730-617-44
; Sequence 44, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shinkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: NO. US20020068279A1e1 Proteins and Nucleic Acids Encoding the Sam
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730.617
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-730-617-44

Query Match 76.9%; Score 40; DB 10; Length 113;
Best Local Similarity 77.8%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 LPALPQVVC 10
||| :|||
Db 63 LPAIPQVVC 71

RESULT 15

US-09-730-617-41
; Sequence 41, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shinkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: NO. US20020068279A1e1 Proteins and Nucleic Acids Encoding the
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730.617
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-730-617-41

Query Match 71.2%; Score 37; DB 10; Length 99;
Best Local Similarity 60.0%; Pred. No. 5.7;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
:|| :|||
Db 48 ILPPMPQVVC 57

RESULT 16

US-09-730-617-47
; Sequence 47, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shinkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: NO. US20020068279A1e1 Proteins and Nucleic Acids Encoding the
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09/730.617
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-730-617-47

```
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Bos taurus
; US-09-730-617-47

Query Match          71.2%   Score 37; DB 10; Length 141;
Best Local Similarity 60.0%; Pred. No. 8.2;
Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 0;

QY 1 VLPALPQVVC 10
   :||: || ||
Db 68 ILPPMPQVVC 77

RESULT 17
US-09-730-617-48
; Sequence 48, Application US/09730617
; Patent No. US20020068279A1
; GENERAL INFORMATION:
; APPLICANT: Burgess, Catherine E
; APPLICANT: Prayaga, Sudhirdas K
; APPLICANT: Shimkets, Richard A
; APPLICANT: Rastelli, Luca
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Mezes, Peter S
; TITLE OF INVENTION: No. US20020068279A1e1 Proteins and Nucleic Acids Encoding the Sam
; FILE REFERENCE: 15966-609
; CURRENT APPLICATION NUMBER: US/09730,617
; CURRENT FILING DATE: 2000-12-05
; PRIOR APPLICATION NUMBER: 60/169,056
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/169,886
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/169,866
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/170,252
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: 60/175,740
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Ovis aries
; US-09-730-617-48

Query Match          71.2%   Score 37; DB 10; Length 141;
Best Local Similarity 60.0%; Pred. No. 8.2;
Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 0;

QY 1 VLPALPQVVC 10
   :||: || ||
Db 68 ILPPMPQVVC 77

RESULT 18
US-09-969-528-10
; Sequence 10, Application US/09969528
; Patent No. US20020150567A1
; GENERAL INFORMATION:
; APPLICANT: Pot, David A.
; APPLICANT: Williams, Lewis T.
; APPLICANT: Jefferson, Anne Bennett
; APPLICANT: Majerus, Philip W.
; TITLE OF INVENTION: No. US20020150567A1e1 Grb2 Associating Protein and Nucleic
```

```
; Acids Encoding Therefor
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/969,528
; FILING DATE: 01-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/560,005
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Dow, Karen B.
; REGISTRATION NUMBER: 29,684
; REFERENCE/DOCKET NUMBER: 2307K-0624000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 654 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..654
; OTHER INFORMATION: /note= "consensus"
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-969-528-10

Query Match          71.2%   Score 37; DB 10; Length 654;
Best Local Similarity 60.0%; Pred. No. 39;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
   :||: || ||
Db 568 LLPLPPVIC 577

RESULT 19
US-09-821-380-9
; Sequence 9, Application US/09821380
; Patent No. US20020064501A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Ahmed
; APPLICANT: Benner, Robert
; APPLICANT: Savelkoul, Josef
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-4799US
; CURRENT APPLICATION NUMBER: US/09/821,380
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/NL99/00313
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/???,???
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: EP 98201695.8
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
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; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fragment of peptide immunoregulator
US-09-821-380-9

Query Match 67.3%; Score 35; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.6e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQ 7
Db 1 VLPALPQ 7

RESULT 20

US-09-821-380-10
; Sequence 10, Application US/09821380
; Patent No. US20020064501A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Ahmed
; APPLICANT: Benner, Robbert
; APPLICANT: Savelkoul, Josef
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-4799US
; CURRENT APPLICATION NUMBER: US/09/821.380
; PRIOR FILING DATE: 2001-03-29
; PRIOR FILING DATE: 1999-05-20
; PRIOR FILING DATE: US 09/???, ???
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: EP 98201695.8
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fragment of peptide immunoregulator
US-09-821-380-10

Query Match 67.3%; Score 35; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.6e+04;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQ 7
Db 2 VLPALPQ 8

RESULT 21

US-09-821-380-4
; Sequence 4, Application US/09821380
; Patent No. US20020064501A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Ahmed
; APPLICANT: Benner, Robbert
; APPLICANT: Savelkoul, Josef
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-4799US
; CURRENT APPLICATION NUMBER: US/09/821.380
; PRIOR FILING DATE: 2001-03-29
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: PCT/NL99/00313
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/???, ???
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: EP 98201695.8
; PRIOR FILING DATE: 1999-05-20

; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fragment of peptide immunoregulator
US-09-821-380-4

Query Match 67.3%; Score 35; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQ 7
Db 4 VLPALPQ 10

RESULT 22

US-09-864-761-44768
; Sequence 44768, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

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; SEQ ID NO 44768
; LENGTH: 67
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC024060.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.63
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.89
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.55
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.62
; OTHER INFORMATION: SWISSPROT HIT: P36774, EVALUE 1.40e-02
; OTHER INFORMATION: EST_HUMAN HIT: AW960705.1, EVALUE 3.00e-33
US-09-864-761-44768

Query Match          65.4%   Score 34;   DB 10;   Length 67;
Best Local Similarity 66.7%   Pred. No. 12;
Matches 6;   Conservative 2;   Mismatches 0;   Gaps 0;

QY  1 VLPALPQVVC 9
    I:I I:I I:I
Db   22 VIPVLPQVM 30

RESULT 23
US-09-864-761-36293
; Sequence 36293, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aomicax-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
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; PRIOR APPLICATION NUMBER: PCT/US01/00663
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
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; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
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; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36293
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL032818.2
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.3
; OTHER INFORMATION: EST_HUMAN HIT: BE974839.1, EVALUE 8.10e-02
; OTHER INFORMATION: SWISSPROT HIT: O30409, EVALUE 1.60e-01
US-09-864-761-36293

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Best Local Similarity 66.7%   Pred. No. 16;
Matches 6;   Conservative 3;   Mismatches 0;   Indels 0;   Gaps 0;

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    I:I I:I I:I
Db   36 LLPALPQML 44

RESULT 24
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; Sequence 14, Application US/09361655
; Patent No. US20020161204A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: LEE, Se-Jin
; APPLICANT: ESQUELA, Aurora F.
; TITLE OF INVENTION: METHODS OF DETECTING LIVER CELLS EXPRESSING GROWTH DIFFERENTIA
; TITLE OF INVENTION: FACTOR-12
; FILE REFERENCE: JHU1220-4
; CURRENT APPLICATION NUMBER: US/09/361,655
; CURRENT FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 08/765,662
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: PCT/ US95/08745
; PRIOR FILING DATE: 1995-07-12
; PRIOR APPLICATION NUMBER: US 08/274,215
; PRIOR FILING DATE: 1994-07-13
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-361-655-14

Query Match          65.4%   Score 34;   DB 9;   Length 350;
Best Local Similarity 60.0%   Pred. No. 67;
Matches 6;   Conservative 1;   Mismatches 3;   Indels 0;   Gaps 0;

QY  1 VLPALPQVVC 10
    I:I I:I I:I
Db   130 VLPTLPGLC 139

RESULT 25
US-09-864-761-36308
; Sequence 36308, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aemica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 36308
LENGTH: 128
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AL035669.28
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
OTHER INFORMATION: EST HUMAN HIT: BF055116.1, EVALUE 2.00e-03
OTHER INFORMATION: SWISSPROT HIT: P40602, EVALUE 9.50e-01
US-09-864-761-36308

Query Match 63.5%; Score 33; DB 10; Length 128;
Best Local Similarity 55.6%; Pred. No. 36;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 2 LPALPQVVC 10
Db 52 MPSLPQLHC 60

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Job time : 5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:36:10 ; Search time 103.75 seconds
(without alignments)
62.143 Million cell updates/sec

Title: US-09-821-380-3
Perfect score: 52
Sequence: 1 VLPALPQVVC 10

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Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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3	52	100.0	11	1	PCT-US97-11202A-28
4	52	100.0	11	16	US-09-220-415-28
5	52	100.0	11	20	US-09-675-362-28
6	52	100.0	11	20	US-09-675-776-28

7	52	100.0	11	20	US-09-677-152-28	Sequence 28, Appl
8	52	100.0	12	1	PCT-US97-11202-22	Sequence 22, Appl
9	52	100.0	12	1	PCT-US97-11202A-22	Sequence 22, Appl
10	52	100.0	12	10	US-08-669-654-21	Sequence 21, Appl
11	52	100.0	12	11	US-08-709-933-22	Sequence 22, Appl
12	52	100.0	12	16	US-09-220-415-22	Sequence 22, Appl
13	52	100.0	12	20	US-09-675-362-22	Sequence 22, Appl
14	52	100.0	12	20	US-09-675-776-22	Sequence 22, Appl
15	52	100.0	12	20	US-09-677-152-22	Sequence 22, Appl
16	52	100.0	12	24	US-10-050-875-22	Sequence 22, Appl
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18	52	100.0	13	1	PCT-US97-11202A-6	Sequence 6, Appl
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21	52	100.0	13	16	US-09-220-415-6	Sequence 6, Appl
22	52	100.0	13	20	US-09-675-362-6	Sequence 6, Appl
23	52	100.0	13	20	US-09-675-776-6	Sequence 6, Appl
24	52	100.0	13	20	US-09-677-152-6	Sequence 6, Appl
25	52	100.0	13	22	US-09-821-380-2	Sequence 2, Appl
26	52	100.0	13	24	US-10-050-875-6	Sequence 6, Appl
27	52	100.0	14	1	PCT-US97-11202-12	Sequence 12, Appl
28	52	100.0	14	1	PCT-US97-11202-18	Sequence 18, Appl
29	52	100.0	14	1	PCT-US97-11202-26	Sequence 26, Appl
30	52	100.0	14	1	PCT-US97-11202A-12	Sequence 12, Appl
31	52	100.0	14	1	PCT-US97-11202A-18	Sequence 18, Appl
32	52	100.0	14	1	PCT-US97-11202A-26	Sequence 26, Appl
33	52	100.0	14	10	US-08-669-654-7	Sequence 7, Appl
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36	52	100.0	14	11	US-08-709-933-26	Sequence 26, Appl
37	52	100.0	14	16	US-09-220-415-12	Sequence 12, Appl
38	52	100.0	14	16	US-09-220-415-18	Sequence 18, Appl
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45	52	100.0	14	20	US-09-675-776-26	Sequence 26, Appl
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51	52	100.0	14	24	US-10-050-875-26	Sequence 26, Appl
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53	52	100.0	15	1	PCT-US97-11202A-37	Sequence 37, Appl
54	52	100.0	15	16	US-09-220-415-37	Sequence 37, Appl
55	52	100.0	15	20	US-09-675-362-37	Sequence 37, Appl
56	52	100.0	15	20	US-09-675-776-37	Sequence 37, Appl
57	52	100.0	15	20	US-09-677-152-37	Sequence 37, Appl
58	52	100.0	17	15	US-09-101-283-8	Sequence 8, Appl
59	52	100.0	17	22	US-09-821-380-1	Sequence 1, Appl
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61	52	100.0	20	1	PCT-US00-27741-5	Sequence 5, Appl
62	52	100.0	20	1	PCT-US00-27741-23	Sequence 23, Appl
63	52	100.0	20	1	PCT-US97-11202-34	Sequence 34, Appl
64	52	100.0	20	1	PCT-US97-11202A-34	Sequence 34, Appl
65	52	100.0	20	8	US-08-406-916B-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-821-380-3
; Sequence 3, Application US/09821380
; GENERAL INFORMATION:
; APPLICANT: Khan, Ahmed
; APPLICANT: Benner, Robbert
; APPLICANT: Savelkoul, Josef
; TITLE OF INVENTION: IMMUNOREGULATOR
; FILE REFERENCE: 2183-4799US

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; CURRENT APPLICATION NUMBER: US/09/821,380
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: PCT/NL99/00313
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: US 09/???,???
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: EP 98201695.8
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98202706.2
; PRIOR FILING DATE: 1999-08-12
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Fragment of peptide immunoregulator
US-09-821-380-3

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Matches 10; Conservative 0; Mismatches 0; Gaps 0;

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Db 1 VLPALPQVVC 10

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US97-11202-28

Query Match          100.0%; Score 52; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 VLPALPQVVC 11

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US97-11202-28

RESULT 3
PCT-US97-11202A-28
; Sequence 28, Application PC/TUS9711202A
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF
; TITLE OF INVENTION: HIV INFECTION BY ADMINISTRATION OF
; TITLE OF INVENTION: DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/11202A
; FILING DATE: 24-JUN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/709,948
; FILING DATE: 09-SEP-1996
; APPLICATION NUMBER: USSN 08/669,681
; FILING DATE: 24-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNTE
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US97-11202A-28

Query Match          100.0%; Score 52; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 VLPALPQVVC 11

; STRANDEDNESS: single
; TOPOLOGY: linear
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PCT-US97-11202-28

Query Match          100.0%; Score 52; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 2 VLPALPQVVC 11

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US97-11202-28

RESULT 4
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; Sequence 28, Application PC/TUS9711202A
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF
; TITLE OF INVENTION: HIV INFECTION BY ADMINISTRATION OF
; TITLE OF INVENTION: DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/11202
; FILING DATE: 24-JUN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/709,948
; FILING DATE: 09-SEP-1996
; APPLICATION NUMBER: USSN 08/669,681
; FILING DATE: 24-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNTE
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
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US-09-220-415-28
; Sequence 28, Application US/09220415
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: Therapeutic Polypeptides from (-hCG and Derivatives
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property/Technology Law
; STREET: P.O. Box 14329
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/220,415
; FILING DATE: 24-DEC-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/11210
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11209
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11448
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11202
; FILING DATE: 24-JUN-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Steven J. Hultquist
; REGISTRATION NUMBER: 28,021
; REFERENCE/DOCKET NUMBER: 4115-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-419-9350
; TELEFAX: 919-419-9354
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-220-415-28

Query Match 100.0%; Score 52; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
Db 2 VLPALPQVVC 11
|||||

RESULT 5
US-09-675-362-28
; Sequence 28, Application US/09675362
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHOD FOR TREATING CANCER
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property/Technology Law
; STREET: P.O. Box 14329
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
```

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ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/675,362
FILING DATE: 29-Sep-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/220,415
FILING DATE: 24-DEC-1998
APPLICATION NUMBER: PCT/US97/11210
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11209
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11448
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11202
FILING DATE: 24-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Marianne Fuller
REGISTRATION NUMBER: 39,983
REFERENCE/DOCKET NUMBER: 4115-116 DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-419-9350
TELEFAX: 919-419-9354
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-675-362-28

Query Match 100.0%; Score 52; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
Db 2 VLPALPQVVC 11
|||||

RESULT 6
US-09-675-776-28
; Sequence 28, Application US/09675776
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHOD FOR PROMOTING HEMATOPOIESIS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property/Technology Law
; STREET: P.O. Box 14329
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/675,776
; FILING DATE: 29-Sep-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
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APPLICATION NUMBER: 09/220,415
FILING DATE: 24-DEC-1998
APPLICATION NUMBER: PCT/US97/11210
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11209
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11448
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11202
FILING DATE: 24-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Marianne Fuieler
REGISTRATION NUMBER: 39,983
REFERENCE/DOCKET NUMBER: 4115-116 DIV2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-419-9350
TELEFAX: 919-419-9354
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-675-776-28

Query Match 100.0%; Score 52; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
| | | | | | | | | | | |
Db 2 VLPALPQVVC 11

RESULT 7
US-09-677-152-28
Sequence 28, Application US/09677152
GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
Bryant, Joseph
Lunardi-Iskandar, Yanto
TITLE OF INVENTION: Therapeutic Fractions of Sources of hCG
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Intellectual Property/Technology Law
STREET: P.O. Box 14329
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/677,152
FILING DATE: 02-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/11210
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11209
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11448
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11202
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: USSN 09/220,415
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Steven J. Hultquist
REGISTRATION NUMBER: 28,021
REFERENCE/DOCKET NUMBER: 4115-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-419-9350
TELEFAX: 919-419-9354
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-677-152-28

Query Match 100.0%; Score 52; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
| | | | | | | | | | | |
Db 2 VLPALPQVVC 11

RESULT 8
PCT-US97-11202-22
Sequence 22, Application PCT/US9711202
GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
APPLICANT: Bryant, Joseph
Lunardi-Iskandar, Yanto
TITLE OF INVENTION: TREATMENT AND PREVENTION OF
TITLE OF INVENTION: HIV INFECTION BY ADMINISTRATION OF
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/11202
FILING DATE: 24-JUN-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/709,948
FILING DATE: 09-SEP-1996
APPLICATION NUMBER: USSN 08/669,681
FILING DATE: 24-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8769-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US97-11202-22

Query Match 100.0%; Score 52; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
 |1111111111|
 Db 2 VLPALPQVVC 11

RESULT 9

PCT-US97-11202A-22
 ; Sequence 22, Application PC/TUS9711202A
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallo, Robert C.
 ; APPLICANT: Bryant, Joseph
 ; APPLICANT: Lunardi-Iskandar, Yanto
 ; TITLE OF INVENTION: TREATMENT AND PREVENTION OF
 ; TITLE OF INVENTION: HIV INFECTION BY ADMINISTRATION OF
 ; TITLE OF INVENTION: DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10036/2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US97/11202A
 FILING DATE: 24-JUN-1997

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 08/709,948
 FILING DATE: 09-SEP-1996

APPLICATION NUMBER: USSN 08/669,681
 FILING DATE: 24-JUN-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 8769-024
 TELEPHONE: 212-790-9090
 TELEFAX: 212-869-8864

TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: peptide
 PCT-US97-11202A-22

Query Match 100.0%; Score 52; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
 |1111111111|
 Db 2 VLPALPQVVC 11

RESULT 10

US-08-669-654-21
 ; Sequence 21, Application US/08669654
 ; GENERAL INFORMATION:
 ; APPLICANT: Gallo, Robert C.
 ; APPLICANT: Bryant, Joseph
 ; APPLICANT: Lunardi-Iskandar, Yanto

; TITLE OF INVENTION: METHODS OF PROMOTING HEMATOPOIESIS USING
 ; TITLE OF INVENTION: DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA

ZIP: 10036-2711
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/669,654
 FILING DATE: 24-JUN-1996

CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie
 REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 8769-004
 TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

MOLECULE TYPE: peptide
 US-08-669-654-21

Query Match 100.0%; Score 52; DB 10; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
 |1111111111|
 Db 2 VLPALPQVVC 11

RESULT 11

US-08-709-933-22
 ; Sequence 22, Application US/08709933
 ; GENERAL INFORMATION:

APPLICANT: Gallo, Robert C.
 APPLICANT: Bryant, Joseph

APPLICANT: Lunardi-Iskandar, Yanto
 TITLE OF INVENTION: METHODS OF TREATMENT OF WASTING SYNDROME

TITLE OF INVENTION: BASED ON ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC
 TITLE OF INVENTION: GONADOTROPIN

NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA

ZIP: 10036-2711
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/709,933
 FILING DATE: 09-SEP-1996

CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:

NAME: Misrock, S. Leslie

REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8769-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-709-933-22

Query Match 100.0%; Score 52; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 2 VLPALPQVVC 11

RESULT 12

US-09-220-415-22
Sequence 22, Application US/09220415

GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
APPLICANT: Bryant, Joseph
APPLICANT: Lunardi-Iskandar, Yanto
TITLE OF INVENTION: Therapeutic Polypeptides from (-hCG and Derivatives
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Intellectual Property/Technology Law
STREET: P.O. Box 14329
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220,415
FILING DATE: 24-DEC-1998
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/11210
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11209
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11448
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11202
FILING DATE: 24-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Steven J. Hultquist
REGISTRATION NUMBER: 28,021
REFERENCE/DOCKET NUMBER: 4115-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-419-9350
TELEFAX: 919-419-9354
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-220-415-22

Query Match 100.0%; Score 52; DB 16; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 2 VLPALPQVVC 11

RESULT 13

US-09-675-362-22
Sequence 22, Application US/09675362

GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
APPLICANT: Bryant, Joseph
APPLICANT: Lunardi-Iskandar, Yanto
TITLE OF INVENTION: METHOD FOR TREATING CANCER
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Intellectual Property/Technology Law
STREET: P.O. Box 14329
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/675,362
FILING DATE: 29-Sep-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/220,415
FILING DATE: 24-DEC-1998
APPLICATION NUMBER: PCT/US97/11210
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11209
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11448
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11202
FILING DATE: 24-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Marianne Fuierer
REGISTRATION NUMBER: 39,983
REFERENCE/DOCKET NUMBER: 4115-116 DIV3

TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-419-9350
TELEFAX: 919-419-9354
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-675-362-22

Query Match 100.0%; Score 52; DB 20; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 2 VLPALPQVVC 11

RESULT 14

US-09-675-776-22
Sequence 22, Application US/09675776
GENERAL INFORMATION:

```

;
; APPLICANT: Gallo, Robert C.
; Bryant, Joseph
; Lunardi-Iskandar, Yanto
;
; TITLE OF INVENTION: METHOD FOR PROMOTING HEMATOPOIESIS
;
; NUMBER OF SEQUENCES: 37
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property/Technology Law
; STREET: P.O. Box 14329
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PatentIn
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/675,776
; FILING DATE: 29-Sep-2000
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/220,415
; FILING DATE: 24-DEC-1998
; APPLICATION NUMBER: PCT/US97/11210
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11209
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11448
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11202
; FILING DATE: 24-JUN-1998
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Marianne Fuierer
; REGISTRATION NUMBER: 39,983
; REFERENCE/DOCKET NUMBER: 4115-116 DIV2
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-419-9350
; TELEFAX: 919-419-9354
;
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
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; US-09-675-776-22
;
; Query Match 100.0%; Score 52; DB 20; Length 12;
; Best Local Similarity 100.0%; Pred. No. 0.13;
; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 VLPALPQVVC 10
; Db 2 VLPALPQVVC 11
;
; RESULT 15
; Sequence 22, Application US/09677152
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; Bryant, Joseph
; Lunardi-Iskandar, Yanto
;
; TITLE OF INVENTION: Therapeutic Fractions of Sources of hCG
;
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property/Technology Law
; STREET: P.O. Box 14329
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
;

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PatentIn
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/677,152
; FILING DATE: 02-Oct-2000
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/11210
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11209
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11448
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: PCT/US97/11202
; FILING DATE: 24-JUN-1998
; APPLICATION NUMBER: USSN 09/220,415
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Steven J. Hultquist
; REGISTRATION NUMBER: 28,021
; REFERENCE/DOCKET NUMBER: 4115-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-419-9350
; TELEFAX: 919-419-9354
;
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
;
; US-09-677-152-22
;
; Query Match 100.0%; Score 52; DB 20; Length 12;
; Best Local Similarity 100.0%; Pred. No. 0.13;
; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 VLPALPQVVC 10
; Db 2 VLPALPQVVC 11
;
; RESULT 16
; US-10-050-875-22
; Sequence 22, Application US/10050875
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; Bryant, Joseph
; Lunardi-Iskandar, Yanto
;
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF HIV INFECTION
; BY ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC GONA
;
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/050,875
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,948
;

```

;; FILING DATE: 09-SEP-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Misrock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 8769-016
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 12 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-050-875-22

Query Match 100.0%; Score 52; DB 24; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.13; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0;

Qy 1 VLPALPQVVC 10
Db 2 VLPALPQVVC 11

RESULT 17
PCT-US97-11202-6
; Sequence 6, Application PC/TUS9711202
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF
; TITLE OF INVENTION: HIV INFECTION BY ADMINISTRATION OF
; TITLE OF INVENTION: DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/11202
; FILING DATE: 24-JUN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/709,948
; FILING DATE: 09-SEP-1996
; APPLICATION NUMBER: USSN 08/669,681
; FILING DATE: 24-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

PCT-US97-11202-6

Query Match 100.0%; Score 52; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
Db 4 VLPALPQVVC 13

RESULT 18
PCT-US97-11202A-6
; Sequence 6, Application PC/TUS9711202A
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Bryant, Joseph
; APPLICANT: Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: TREATMENT AND PREVENTION OF
; TITLE OF INVENTION: HIV INFECTION BY ADMINISTRATION OF
; TITLE OF INVENTION: DERIVATIVES OF HUMAN CHORIONIC GONADOTROPIN
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/11202A
; FILING DATE: 24-JUN-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/709,948
; FILING DATE: 09-SEP-1996
; APPLICATION NUMBER: USSN 08/669,681
; FILING DATE: 24-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 8769-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US97-11202A-6

Query Match 100.0%; Score 52; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
Db 4 VLPALPQVVC 13

RESULT 19
US-08-669-654-6
; Sequence 6, Application US/08669654
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.

APPLICANT: Bryant, Joseph
APPLICANT: Lunardi-Iskandar, Yanto
TITLE OF INVENTION: METHODS OF PROMOTING HEMATOPOIESIS USING
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,654
FILING DATE: 24-JUN-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8769-004
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-669-654-6

Query Match 100.0%; Score 52; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
Db 4 VLPALPQVVC 13

RESULT 20
US-08-709-933-6
Sequence 6, Application US/08709933
GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
APPLICANT: Bryant, Joseph
APPLICANT: Lunardi-Iskandar, Yanto
TITLE OF INVENTION: METHODS OF TREATMENT OF WASTING SYNDROME
TITLE OF INVENTION: BASED ON ADMINISTRATION OF DERIVATIVES OF HUMAN CHORIONIC
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,933
FILING DATE: 09-SEP-1996
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 8769-019
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNTE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-709-933-6

Query Match 100.0%; Score 52; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
Db 4 VLPALPQVVC 13

RESULT 21
US-09-220-415-6
Sequence 6, Application US/09220415
GENERAL INFORMATION:
APPLICANT: Gallo, Robert C.
APPLICANT: Bryant, Joseph
APPLICANT: Lunardi-Iskandar, Yanto
TITLE OF INVENTION: Therapeutic Polypeptides from (-hCG and Derivatives
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Intellectual Property/Technology Law
STREET: P.O. Box 14329
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/11210
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11209
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11448
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11202
FILING DATE: 24-JUN-1998
ATTORNEY/AGENT INFORMATION:
NAME: Steven J. Hultquist
REGISTRATION NUMBER: 28,021
REFERENCE/DOCKET NUMBER: 4115-116
TELEPHONE: 919-419-9350
TELEFAX: 919-419-9354
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-220-415-6

Query Match 100.0%; Score 52; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.15; 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVC 10
| | | | | | | | | |
Db 4 VLPALPQVC 13

RESULT 22

US-09-675-362-6
; Sequence 6, Application US/09675362
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; Bryant, Joseph
; Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHOD FOR TREATING CANCER
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property/Technology Law
; STREET: P.O. Box 14329
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/675.362
FILING DATE: 29-Sep-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/220,415
FILING DATE: 24-DEC-1998

APPLICATION NUMBER: PCT/US97/11210
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11209
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11448
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11202
FILING DATE: 24-JUN-1998

ATTORNEY/AGENT INFORMATION:
NAME: Marianne Fuierer
REGISTRATION NUMBER: 39,983
REFERENCE/DOCKET NUMBER: 4115-116 DIV3

TELEPHONE: 919-419-9350
TELEFAX: 919-419-9354
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Query Match 100.0%; Score 52; DB 20; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVC 10
| | | | | | | | | |
Db 4 VLPALPQVC 13

RESULT 23

US-09-675-776-6

US-09-675-362-6
; Sequence 6, Application US/09675362
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; Bryant, Joseph
; Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHOD FOR TREATING CANCER
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property/Technology Law
; STREET: P.O. Box 14329
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/675.362
FILING DATE: 29-Sep-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/220,415
FILING DATE: 24-DEC-1998
APPLICATION NUMBER: PCT/US97/11210
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11209
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11448
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11202
FILING DATE: 24-JUN-1998

ATTORNEY/AGENT INFORMATION:
NAME: Marianne Fuierer
REGISTRATION NUMBER: 39,983
REFERENCE/DOCKET NUMBER: 4115-116 DIV3

TELEPHONE: 919-419-9350
TELEFAX: 919-419-9354
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Query Match 100.0%; Score 52; DB 20; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-675-776-6
; Sequence 6, Application US/09675776
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; Bryant, Joseph
; Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: METHOD FOR PROMOTING HEMATOPOIESIS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property/Technology Law
; STREET: P.O. Box 14329
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/675.776
FILING DATE: 29-Sep-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/220,415
FILING DATE: 24-DEC-1998
APPLICATION NUMBER: PCT/US97/11210
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11209
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11448
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11202
FILING DATE: 24-JUN-1998

ATTORNEY/AGENT INFORMATION:
NAME: Marianne Fuierer
REGISTRATION NUMBER: 39,983
REFERENCE/DOCKET NUMBER: 4115-116 DIV2

TELEPHONE: 919-419-9350
TELEFAX: 919-419-9354
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Query Match 100.0%; Score 52; DB 20; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVC 10
| | | | | | | | | |
Db 4 VLPALPQVC 13

RESULT 24

US-09-677-152-6

US-09-677-152-6
; Sequence 6, Application US/09677152
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; Bryant, Joseph
; Lunardi-Iskandar, Yanto
; TITLE OF INVENTION: Therapeutic Fractions of Sources of hCG
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Intellectual Property/Technology Law
; STREET: P.O. Box 14329
; CITY: Research Triangle Park
; STATE: NC

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/675.776
FILING DATE: 29-Sep-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/220,415
FILING DATE: 24-DEC-1998
APPLICATION NUMBER: PCT/US97/11210
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11209
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11448
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11202
FILING DATE: 24-JUN-1998

ATTORNEY/AGENT INFORMATION:
NAME: Marianne Fuierer
REGISTRATION NUMBER: 39,983
REFERENCE/DOCKET NUMBER: 4115-116 DIV2

TELEPHONE: 919-419-9350
TELEFAX: 919-419-9354
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Query Match 100.0%; Score 52; DB 20; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVC 10
| | | | | | | | | |
Db 4 VLPALPQVC 13

COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PatentIn
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/677,152
FILING DATE: 02-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/11210
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11209
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11448
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: PCT/US97/11202
FILING DATE: 24-JUN-1998
APPLICATION NUMBER: USSN 09/220,415
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Steven J. Hultquist
REGISTRATION NUMBER: 28,021
REFERENCE/DOCKET NUMBER: 4115-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-419-9350
TELEFAX: 919-419-9354
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-677-152-6
Query Match 100.0%; Score 52; DB 20; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLPALPQVVC 10
Db 4 VLPALPQVVC 13
Search completed: December 4, 2002, 11:36:17
Job time : 103.75 secs
OTHER INFORMATION: Fragment of peptide immunoregulator
US-09-821-380-2
Query Match 100.0%; Score 52; DB 22; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLPALPQVVC 10
Db 4 VLPALPQVVC 13
Search completed: December 4, 2002, 11:36:17
Job time : 103.75 secs
OTHER INFORMATION: Fragment of peptide immunoregulator
US-09-821-380-2
Query Match 100.0%; Score 52; DB 20; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLPALPQVVC 10
Db 4 VLPALPQVVC 13
RESULT 25
US-09-821-380-2
Sequence 2, Application US/09821380
GENERAL INFORMATION:
APPLICANT: Khan, Ahmed
APPLICANT: Benner, Robert
APPLICANT: Savelkoul, Josef
TITLE OF INVENTION: IMMUNOREGULATOR
FILE REFERENCE: 2183-4799US
CURRENT APPLICATION NUMBER: US/09/821,380
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: PCT/NL99/00313
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: US 09/??? , ???
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: EP 98201695.8
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: EP 98202706.2
PRIOR FILING DATE: 1999-08-12
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 13
TYPE: PRT
ORGANISM: Unknown
FEATURE:


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RESULT 2
US-10-029-206A-34
; Sequence 34, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligopeptide
US-10-029-206A-34

Query Match      100.0%; Score 52; DB 6; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
   |||||
Db 4 VLPALPQVVC 13

RESULT 3
US-10-029-206A-165
; Sequence 165, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 165
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HLA-DRB1*0101
US-10-029-206A-165

Query Match      100.0%; Score 52; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
   |||||
Db 4 VLPALPQVVC 13

RESULT 4
US-10-029-206A-44
; Sequence 44, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: peptide
US-10-029-206A-44

Query Match      100.0%; Score 52; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
   |||||
Db 8 VLPALPQVVC 17

RESULT 5
US-10-029-206A-97
; Sequence 97, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: A1188872
US-10-029-206A-97

Query Match      100.0%; Score 52; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
   |||||
Db 8 VLPALPQVVC 17

RESULT 6
US-10-029-206A-174
; Sequence 174, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 174
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The (Xaa) at position 2 indicates an unknown amino acid
US-10-029-206A-174

Query Match      100.0%; Score 52; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
   |||||
Db 8 VLPALPQVVC 17
```

; SEQ ID NO 174
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NMPF-71
; US-10-029-206A-174

Query Match 100.0%; Score 52; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
| | | | | | | |
Db 8 VLPALPQVVC 17

RESULT 7
US-09-724-676-63209
; Sequence 63209, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63209
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-724-676-63209

Query Match 100.0%; Score 52; DB 5; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
| | | | | | | |
Db 66 VLPALPQVVC 75

RESULT 8
US-09-724-676A-63209
; Sequence 63209, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 63209
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-724-676A-63209

Query Match 100.0%; Score 52; DB 5; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
| | | | | | | |
Db 66 VLPALPQVVC 75

RESULT 9
US-10-187-176-7
; Sequence 7, Application US/10187176

; GENERAL INFORMATION:
; APPLICANT: Ji, Tae H.
; TITLE OF INVENTION: Agents and Methods for Modulating Interactions Between
; FILE REFERENCE: 028750-221
; CURRENT APPLICATION NUMBER: US/10/187,176
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/301,834
; PRIOR FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 165
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CG amino acid sequence
; US-10-187-176-7

Query Match 100.0%; Score 52; DB 6; Length 165;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
| | | | | | | |
Db 68 VLPALPQVVC 77

RESULT 10
US-10-029-206A-99
; Sequence 99, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 99
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: A1126906
; US-10-029-206A-99

Query Match 96.2%; Score 50; DB 6; Length 17;
Best Local Similarity 90.0%; Pred. No. 0.014;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
| | | | | | | |
Db 8 VLPALPQVVC 17

RESULT 11
US-10-029-206A-133
; Sequence 133, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; NUMBER OF SEQ ID NOS: 175

```
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 133
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P01229/LSHB HUMAN
US-10-029-206A-133

Query Match          90.4%; Score 47; DB 6; Length 17;
Best Local Similarity 90.0%; Pred. No. 0.046;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 VLPALPQVVC 10
   ||| |||||
Db 8 VLPLPQVVC 17

RESULT 12
US-10-187-176-8
; Sequence 8, Application US/10187176
; GENERAL INFORMATION:
; APPLICANT: Ji, Inhae
; TITLE OF INVENTION: Agents and Methods for Modulating Interactions Between
; TITLE OF INVENTION: Gonadotropin Hormones and Receptors
; FILE REFERENCE: 028750-221
; CURRENT APPLICATION NUMBER: US/10/187,176
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/301,834
; PRIOR FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CG amino acid sequence
US-10-187-176-8

Query Match          90.4%; Score 47; DB 6; Length 127;
Best Local Similarity 90.0%; Pred. No. 0.32;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 VLPALPQVVC 10
   ||| |||||
Db 54 VLPLPQVVC 63

RESULT 13
US-10-029-206A-139
; Sequence 139, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: swissnew/P07434/CGHB PAPAN
US-10-029-206A-139

Query Match          84.6%; Score 44; DB 6; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.15;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 VLPALPQVVC 10
   ||| |||||
Db 8 VLPPVPQVVC 17

RESULT 14
US-10-029-206A-158
; Sequence 158, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 158
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HLA molecule
US-10-029-206A-158

Query Match          82.7%; Score 43; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVV 9
   ||| |||||
Db 1 VLPALPQVV 9

RESULT 15
US-10-029-206A-164
; Sequence 164, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 164
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HLA-DRB1*0101
US-10-029-206A-164

Query Match          82.7%; Score 43; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVV 9
   ||| |||||
Db 7 VLPALPQVV 15
```

```
RESULT 16
US-10-029-206A-157
; Sequence 157, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 157
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HLA molecule
; OTHER INFORMATION: type I (A_0201)
US-10-029-206A-157

Query Match          75.0%; Score 39; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQV 8
Db 2 VLPALPQV 9

RESULT 17
US-10-029-206A-166
; Sequence 166, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 166
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HLA-DRB1*0301
; OTHER INFORMATION: (DR17) 15-mers
US-10-029-206A-166

Query Match          75.0%; Score 39; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQV 8
Db 8 VLPALPQV 15

RESULT 18
US-10-029-206A-29
; Sequence 29, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligopeptide
US-10-029-206A-29

Query Match          67.3%; Score 35; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQ 7
Db 1 VLPALPQ 7

RESULT 19
US-10-029-206A-33
; Sequence 33, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: oligopeptide
US-10-029-206A-33

Query Match          67.3%; Score 35; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQ 7
Db 2 VLPALPQ 8

RESULT 20
US-10-029-206A-49
; Sequence 49, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Description of Artificial Sequence: peptide
OTHER INFORMATION: signalling molecule
US-10-029-206A-49

Query Match 67.3%; Score 35; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQ 7
| | | | | | |
DB 4 VLPALPQ 10

RESULT 21
US-10-029-206A-171
; Sequence 171, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 171
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: NMPF-70
; OTHER INFORMATION: peptide
US-10-029-206A-171

Query Match 67.3%; Score 35; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQ 7
| | | | | | |
DB 8 VLPALPQ 14

RESULT 22
PCT-US02-32727-9060
; Sequence 9060, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 9060
; LENGTH: 68
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-9060

Query Match 67.3%; Score 35; DB 1; Length 68;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQ 7
| | | | | | |
DB 7 VLPALPQ 13

RESULT 23
US-10-029-206A-108
; Sequence 108, Application US/10029206A
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Benner, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 2183-5222US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/821,380
; PRIOR FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 108
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Mm.129320.2
US-10-029-206A-108

Query Match 65.4%; Score 34; DB 6; Length 14;
Best Local Similarity 50.0%; Pred. No. 6.6;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
| | | | | | |
DB 5 VVPMPLPRLC 14

RESULT 24
PCT-US02-32727-21726
; Sequence 21726, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siqing
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Darrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acne
; FILE REFERENCE: 210121.514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 21726
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-21726

Query Match 65.4%; Score 34; DB 1; Length 117;
Best Local Similarity 50.0%; Pred. No. 52;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
|:|:|:|:|
Db 2 VIPSLPRTCC 11

RESULT 25

US-10-264-237-1627
; Sequence 1627, Application US/10264237
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 1627
; LENGTH: 142
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (70)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (139)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (140)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-1627

Query Match 65.4%; Score 34; DB 6; Length 142;
Best Local Similarity 66.7%; Pred. No. 63;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPALPQVVC 10
|:|:|:|:|
Db 81 LPAAPALVC 89

Search completed: December 4, 2002, 11:36:52
Job time : 8.25 secs

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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:23:55 ; Search time 9 Seconds
(without alignments)
106.816 Million cell updates/sec

Title: us-09-821-380-3
Perfect score: 52
Sequence: 1 VLPALPQVVC 10

Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : PIR_73:**

1: pir1:**
2: pir2:**
3: pir3:**
4: pir4:**

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	145	2	I37231
2	52	100.0	165	1	KTHUB
3	47	90.4	141	1	UTHUB
4	44	84.6	165	1	KTBAB
5	40	76.9	169	1	KTHOB
6	37	71.2	141	1	UTSHB
7	37	71.2	141	1	UTSHB
8	37	71.2	686	1	S28050
9	37	71.2	817	2	T16409
10	37	71.2	969	2	S54594
11	36	69.2	304	2	T02911
12	36	69.2	351	2	T19284
13	35	67.3	102	2	T23320
14	35	67.3	256	2	B83612
15	35	67.3	447	2	AE0094
16	35	67.3	591	2	I65981
17	35	67.3	610	2	H71503
18	34	65.4	80	2	I63235
19	34	65.4	119	2	A61465
20	34	65.4	138	2	S00512
21	34	65.4	139	2	I52320
22	34	65.4	141	1	UTRTB
23	34	65.4	141	1	UTPCB
24	34	65.4	141	2	JC4527
25	34	65.4	243	2	D64300
26	34	65.4	249	2	S51621
27	34	65.4	276	2	T49123
28	34	65.4	284	2	AC0572
29	34	65.4	310	2	A41776

30 34 65.4 311 2 S06619
31 34 65.4 313 2 A42853
32 34 65.4 326 2 T36504
33 34 65.4 400 2 E82367
34 34 65.4 509 2 C89491
35 34 65.4 610 2 A81666
36 34 65.4 788 2 AG0786
37 34 65.4 1076 2 C96620
38 34 65.4 1606 2 T49219
39 33 63.5 60 2 AD2865
40 33 63.5 169 2 H82398
41 33 63.5 214 2 D83278
42 33 63.5 280 2 F82704
43 33 63.5 353 2 S69730
44 33 63.5 415 1 A48359
45 33 63.5 419 2 G70602
46 33 63.5 432 2 C95275
47 33 63.5 465 2 AF1858
48 33 63.5 485 2 F4165
49 33 63.5 494 2 A12438
50 33 63.5 505 2 S76722
51 33 63.5 522 2 S77073
52 33 63.5 532 2 S74453
53 33 63.5 535 2 S62437
54 33 63.5 583 2 B82744
55 33 63.5 606 2 S35427
56 33 63.5 671 2 C96546
57 33 63.5 687 2 B70515
58 33 63.5 773 2 A57244
59 33 63.5 1032 2 A11697
60 33 63.5 1139 2 T22811
61 33 63.5 1630 2 A53577
62 33 63.5 2472 2 B83594
63 32 61.5 71 2 I49258
64 32 61.5 118 2 PN0141
65 32 61.5 118 2 PN0139

syndecan-1 precurs
syndecan core prot
probable quinone o
probable multidrug
probable acid-CoA
glucose inhibited
secreted effector
protein T30E16.23
translation initia
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transcription regu
hypothetical prote
glutamyl-tRNA redu
hypothetical prote
probable ABC trans
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UDP-N-acetylmuramo
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conserved hypotet
env polypeptide -
probable GTP-bind
hypothetical prote
transcription elon
alpha-mannosidase
Lin-25 protein - C
ascites sialoglyco
still frameshift p
fibrosin - mouse
lutropin beta chai
lutropin beta chai

ALIGNMENTS

RESULT 1

137231
beta-gonadotropin - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jul-2000

C:Accession: I37231

R:Raimadze, K.; Vamvakopoulos, N.C.; Fiddes, J.C.

Nature 307, 37-40, 1984

A:Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin

A:Reference number: I37231; MUID:84093590; PMID:6690982

A:Accession: I37231

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-145 <RES>

A:Cross-references: EMBL:X00266; NID:G29907; PIDN:CAA25069.1; PID:g1335012

C:Genetics:

A:Introns: 41/3

C:Superfamily: pituitary glycoprotein hormone beta chain

Query Match 100.0%; Score 52; DB 2; Length 145;

Best Local Similarity 100.0%; Pred. No. 0.014;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10

Db 48 VLPALPQVVC 57

RESULT 2

KTHUB

N:Altername names: beta-gonadotropin; chorionic gonadotropin beta chain

C:Species: Homo sapiens (man)
C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 08-Dec-2000
C:Accession: A93230; 159972; 155224; 155250; 170007; 170008; A92303; A92181; A92142; PC1
R:Fiddes, J.C.; Goodman, H.M.
A:Reference number: A93230; MUID:81012134; PMID:6774259
A:Title: The cDNA for the beta-subunit of human chorionic gonadotropin suggests evolution
Nature 286, 684-687, 1980
A:Reference number: A93230
A:Molecule type: mRNA
A:Residues: 1-165 <FID>
A:Cross-references: GB:J00117; GB:M38559; GB:M54963; NID:gi180436; PIDN:AAA96690.1; PID:9
R:Polcastro, P.; O'Witt, C.E.; Hoshina, M.; Fukuoaka, H.; Boothby, M.R.; Boime, I.
J. Biol. Chem. 258, 11492-11499, 1983
A:Title: The beta subunit of human chorionic gonadotropin is encoded by multiple genes.
A:Reference number: 155224; MUID:84008141; PMID:6194155
A:Accession: 159972
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-165 <POL>
A:Cross-references: GB:K03189; NID:gi180450; PIDN:AAA53288.1; PID:gi180453
A:Note: Clone CG-beta-e
A:Accession: 155224
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-23, 'M', 25-136, 'A', 138-165 <PO2>
A:Cross-references: GB:K03183; NID:gi180442; PIDN:AAA53287.1; PID:gi180444
A:Note: Clone CG-beta-a
R:Polcastro, P.F.; Daniels-McQueen, S.; Carle, G.; Boime, I.
J. Biol. Chem. 261, 5907-5916, 1986
A:Title: A map of the hCG beta-LH beta gene cluster.
A:Reference number: 155250; MUID:86195987; PMID:2422163
A:Accession: 155250
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-5 <PO3>
A:Cross-references: GB:M13504; NID:gi180419; PIDN:AAA52005.1; PID:g463088
A:Note: CG-beta-3 gene
A:Accession: 170007
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-5 <PO4>
A:Cross-references: GB:M13505; NID:gi180429; PIDN:AAA52008.1; PID:g463089
A:Note: CG-beta-6 gene
A:Accession: 170008
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-5 <RE5>
A:Cross-references: GB:M13503; NID:gi180432; PIDN:AAA52009.1; PID:g463090
A:Note: CG-beta-7 gene
R:Birden, S.; Fetherston, J.; Canfield, R.; Boime, I.
J. Biol. Chem. 256, 1816-1823, 1981
A:Title: The amino acid sequences of the prepeptides contained in the alpha and beta sub
A:Reference number: A92303; MUID:81117268; PMID:7462224
A:Accession: A92303
A:Molecule type: protein
A:Residues: 1-20 <BIR>
A:Note: The identity of the residue at position 19 could not be determined
R:Morgan, F.J.; Birden, S.; Canfield, R.E.
J. Biol. Chem. 250, 5247-5258, 1975
A:Title: The amino acid sequence of human chorionic gonadotropin. The alpha subunit and
A:Reference number: A92181; MUID:75211304; PMID:1150658
A:Accession: A92181
A:Molecule type: protein
A:Residues: 21-165 <MOR>
R:Carlsen, R.B.; Bahl, O.P.; Swaminathan, N.
J. Biol. Chem. 248, 6810-6827, 1973
A:Reference number: A92142; MUID:74011267; PMID:4795659
A:Accession: A92142
A:Molecule type: protein
A:Residues: 21-22, 'O', 24-73, 'ZL', 76-140, 142-157, 'PB', 160-165, 'SLP', <CAR>
R:Shi, Z.P.; Du, G.G.; Li, W.X.; Liu, X.J.; Li, S.Z.; Xu, Y.S.; Wang, Y.
Chinese Biochem. J. 6, 558-562, 1990
A:Title: The immunological characteristics of the enzymatic fragments of human chorionic

A:Reference number: PC1016
A:Accession: PC1016
A:Molecule type: protein
A:Residues: 21-165 <SHI>
A:Note: article in Chinese with English abstract
R:Birden, S.; Armstrong, E.G.; Kolks, M.A.G.; Cole, L.A.; Agosto, G.M.; Krichevsky, A
Endocrinology 123, 572-583, 1988
A:Title: Structure of the human chorionic gonadotropin beta-subunit fragment from pre
A:Reference number: A61097; MUID:88254680; PMID:2454811
A:Accession: A61097
A:Molecule type: protein
A:Residues: 26-32, 'X', 34-49, 'X', 51-60, 75-112 <B12>
A:Note: this material from pregnancy urine lacks sialic acid in its carbohydrate and h
R:Kardana, A.; Bagshawe, K.D.; Coles, B.; Read, D.; Taylor, M.
Br. J. Cancer 67, 686-692, 1993
A:Title: Characterisation of UGP and its relationship with beta-core fragment.
A:Reference number: A56873; MUID:93228246; PMID:8471426
A:Accession: B36873
A:Molecule type: protein
A:Residues: 26-28, 'X', 30-32, 'X', 34-42, 'X', 44-45, 'X', 47-48, 75-76, 'X', 78-91, 'G', 93-102
A:Experimental source: urine
A:Note: sequence modified after extraction from NCBI backbone
A:Note: this material was designated urinary gonadotropin peptide (peak 2)
R:Lapthorn, A.J.; Harris, D.C.; Littlejohn, A.; Lustbader, J.W.; Canfield, R.E.; Mach
Nature 369, 455-461, 1994
A:Title: Crystal structure of human chorionic gonadotropin.
A:Reference number: A44674; MUID:94261179; PMID:8202136
A:Contents: annotation: X-ray crystallography, 3.0 angstroms; correction of disulfide
R:Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
Nature 307, 37-40, 1984
A:Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin
A:Reference number: 137231; MUID:84093590; PMID:6690982
A:Accession: 137412
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 21-165 <RSS>
A:Cross-references: EMBL:X00265; NID:g31719; PIDN:CAA25068.1; PID:g1335075
C:Genetics:
A:Gene: GDB:CGB
A:Cross-references: GDB:119055; OMIM:118860
A:Map position: 19q13.3-19q13.3
A:Introns: 5/3; 61/3
A:Note: the chorionadotropin beta chain locus contains six genes (or pseudogenes)
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; hormone; pituitary
F:1-20/Domain: signal sequence #status experimental <SIG>
F:21-165/Product: chorionadotropin beta chain #status experimental <MAT>
F:29-77, 43-92, 46-130, 54-108, 58-110, 113-120/Disulfide bonds: #status experimental
F:33, 50/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:138, 150/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:141, 147, 152, 158/Binding site: carbohydrate (Ser) (covalent) #status experimental
Query Match 100.08; Score 52; DB 1; Length 165;
Best Local Similarity 100.08; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLPALPQVVC 10
|||||
DB 68 VLPALPQVVC 77
RESULT 3
UTRUB
lutropin beta chain precursor [validated] - human
N:Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing
C:Species: Homo sapiens (man)
C:Date: 13-Jul-1981 #sequence_revision 24-Nov-1999 #text_change 20-Apr-2001
C:Accession: 137994; 158013; A90604; A92759; A94466; A01497; B94552
R:Talmadge, K.; Vamvakopoulos, N.C.; Fiddes, J.C.
Nature 307, 37-40, 1984
A:Title: Evolution of the genes for the beta subunits of human chorionic gonadotropin
A:Reference number: 137231; MUID:84093590; PMID:6690982
A:Accession: 137994

A:Status: preliminary; translated from GB/EMBL/DBJ; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-141 <TAL>
A:Cross-references: GB:X00264; NID:g34351; PIDN:CAA25067.1; PID:g2292893
R:Weiss, J.; Axelrod, L.; Whitcomb, R.W.; Harris, P.E.; Crowley, W.F.; Jameson, J.L.
N. Engl. J. Med. 326, 179-183, 1992
A:Title: Hypogonadism caused by a single amino acid substitution in the beta subunit of
A:Reference number: F58013; MUID:92085985; PMID:1727547
A:Accession: F58013
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 72-73, 'R', 75-76 <WEI>
A:Cross-references: GB:S71273; NID:g240572; PIDN:AA014960.1; PID:g4262812
A:Note: mutant sequence from patient with hypogonadism
R:Sairam, M.R.; Li, C.H.
Biochim. Biophys. Acta 412, 70-81, 1975
A:Title: Human pituitary lutropin. Isolation, properties, and the complete amino acid se
A:Reference number: A90604; MUID:76082547; PMID:1191677
A:Accession: A90604
A:Molecule type: protein
A:Residues: 21-38, 'Q', 40-75, 77-131, 133-134, 'H', 136-137 <SAI>
R:Shome, B.; Parlow, A.F.
J. Clin. Endocrinol. Metab. 36, 618-621, 1973
A:Title: The primary structure of the hormone-specific, beta subunit of human pituitary
A:Reference number: A92759; MUID:73090987; PMID:4685398
A:Accession: A92759
A:Molecule type: protein
A:Residues: 21-38, 'Q', 40-75, 77-131, 133-134, 'H', 136-137 <SHO>
R:Closset, J.; Hennen, G.; Lequin, R.M.
FEBS Lett. 29, 97-100, 1973
A:Title: Human lutetizing hormone the amino acid sequence of the beta subunit.
A:Reference number: A91389; MUID:73221227; PMID:4719207
A:Contents: annotation; partial sequence
R:Ward, D.N.
unpublished results, cited by Closset, J., Hennen, G., and Lequin, R.M., FEBS Lett. 29,
A:Reference number: A94466
A:Accession: A94466
A:Molecule type: protein
A:Residues: 21-38, 'Q', 40-46 <WAR>
A:Note: 28-Val, 33-Arg, and 35-Thr were also found
R:Shome, B.; Parlow, A.F.
submitted to the Atlas, April 1975
A:Reference number: A94552
A:Contents: annotation; binding site
C:Genetics:
A:Gene: GDB:LHB
A:Cross-references: GDB:119364; OMIM:152780
A:Map position: 19q13.3-19q13.3
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: blocked amino end; glycoprotein; hormone; pituitary
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-141/Product: lutropin beta #status predicted <LTP>
F:21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #stat
F:29-54, 43-77, 46-108, 58-130, 92-120, 110-113/Disulfide bonds: #status predicted
F:50/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 90.4%; Score 47; DB 1; Length 141;
Best Local Similarity 90.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
| | | | | | | | | |
Db 68 VLPPVPQVVC 77

RESULT 4

KTHOB

Choriongonadotropin beta chain precursor - olive baboon
C:Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 28-May-1999
C:Accession: A25808
R:Crawford, R.J.; Tregear, G.W.; Niall, H.D.
Gene 46, 161-169, 1986

A:Title: The nucleotide sequences of baboon chorionic gonadotropin beta-subunit genes
A:Reference number: A25808; MUID:87106851; PMID:2433190
A:Accession: A25808
A:Molecule type: mRNA
A:Residues: 1-165 <CRA>
A:Cross-references: GB:M14966; NID:g176572; PIDN:AAA35383.1; PID:g176573
C:Comment: There are at least five copies of CG-related genes and at least two of the
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; hormone; placenta; pregnancy maintenance
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-165/Product: choriongonadotropin beta chain #status predicted <CGB>
F:29-77, 43-92, 46-130, 54-108, 58-110, 113-120/Disulfide bonds: #status predicted
F:33, 50/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:140, 147, 152/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 84.6%; Score 44; DB 1; Length 165;
Best Local Similarity 80.0%; Pred. No. 0.53;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
| | | | | | | | | |
Db 68 VLPPVPQVVC 77

RESULT 5
KTHOB
choriongonadotropin beta chain precursor - horse
N:Alternate names: chorionic gonadotropin beta chain (CG); lutetizing hormone (LH) b
C:Species: Equus caballus (domestic horse)
C:Date: 14-Nov-1983 #sequence_revision 03-May-1996 #text_change 18-Jun-1999
C:Accession: A41917; A29304; A29305; A01503
R:Sherman, G.B.; Wolfe, M.W.; Farmerie, T.A.; Clay, C.M.; Threadgill, D.S.; Sharp, D.
Mol. Endocrinol. 6, 951-959, 1992
A:Title: A single gene encodes the beta-subunits of equine lutetizing hormone and ch
A:Reference number: A41917; MUID:92357035; PMID:1379674
A:Accession: A41917
A:Molecule type: DNA
A:Residues: 1-169 <SHE>
A:Cross-references: GB:S41704; NID:g252740; PIDN:AAB22775.1; PID:g252741
A:Experimental source: sperm
A:Note: sequence extracted from NCBI backbone (NCBIN:110184, NCBIP:110185)
R:Sugino, H.; Bousfield, G.R.; Moore Jr., W.T.; Ward, D.N.
J. Biol. Chem. 262, 8603-8609, 1987
A:Title: Structural studies on equine glycoprotein hormones. Amino acid sequence of e
A:Reference number: A29304; MUID:87250475; PMID:3298238
A:Accession: A29304
A:Molecule type: protein
A:Residues: 21-169 <SUG>
R:Bousfield, G.R.; Liu, W.K.; Sugino, H.; Ward, D.N.
J. Biol. Chem. 262, 8610-8620, 1987
A:Title: Structural studies on equine glycoprotein hormones. Amino acid sequence of e
A:Reference number: A29305; MUID:87250476; PMID:3298239
A:Accession: A29305
A:Molecule type: protein
A:Residues: 21-169 <BOU>
R:Ward, D.N.; Moore Jr., W.T.; Burleigh, B.D.
J. Protein Chem. 1, 263-280, 1982
A:Title: Structural studies on equine chorionic gonadotropin.
A:Reference number: A01503
A:Accession: A01503
A:Molecule type: protein
A:Residues: 21-40, 'Q', 42-43, 'SK', 46, 'XXX', 51, 'T', 53-64, 'T', 66-96, 'B', 98, 'R', 100-102,
R:Matsui, T.; Mizuochi, T.; Titani, K.; Okinaga, T.; Hoshi, M.; Bousfield, G.R.; Sugii
Biochemistry 33, 14039-14048, 1994
A:Title: Structural analysis of N-linked oligosaccharides of equine chorionic gonadot
A:Reference number: A35952; MUID:95034847; PMID:7524670
A:Contents: annotation; glycosylation
A:Note: horse lutropin and choriongonadotropin beta chains have identical protein chai
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; hormone; pituitary
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-169/Product: choriongonadotropin beta chain #status experimental <MAT>
F:29-77, 43-92, 46-130, 54-108, 58-110, 113-120/Disulfide bonds: #status predicted

F:33/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 76.98; Score 40; DB 1; Length 169;

Best Local Similarity 77.88; Pred. No. 3.1; Mismatches 1; Indels 0; Gaps 0;

Matches 7; Conservative 1; Indels 0; Gaps 0;

QY 2 LPALPQVVC 10

||:|||

Db 69 LPAIPQVVC 77

RESULT 6

UTBOB

Lutropin beta chain precursor - bovine

N:Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 24-Nov-1999

C:Accession: A92534; A92518; A91212; A01499

R:Virgin, J.B.; Silver, B.J.; Thomson, A.R.; Nilsson, J.H.

J. Biol. Chem. 260, 7072-7077, 1985

A:Title: The gene for the beta subunit of bovine luteinizing hormone encodes a gonadotro

A:Reference number: A92534; MUID:85207729; PMID:2987241

A:Accession: A92534

A:Molecule type: DNA

A:Residues: 1-141 <VIR>

A:Cross-references: GB:M11506; NID:g163298; PIDN:AAB59267.1; PID:g163299

R:Maurer, R.A.

J. Biol. Chem. 260, 4684-4687, 1985

A:Title: Analysis of several bovine lutropin beta subunit cDNAs reveals heterogeneity in

A:Reference number: A92518; MUID:85182575; PMID:3838746

A:Accession: A92518

A:Molecule type: mRNA

A:Residues: 3-111, 'S', 113-141 <MAU>

A:Cross-references: GB:M10077; NID:g163300; PIDN:AAA30623.1; PID:g163301

R:Magnulin-Rogister, G.; Hennen, G.

Eur. J. Biochem. 39, 235-253, 1973

A:Title: Luteinizing hormone. The primary structures of the beta-subunit from bovine and

A:Reference number: A91212; MUID:74075724; PMID:4770795

A:Accession: A91212

A:Molecule type: protein

A:Residues: 21-73, 'E', 75-121, 'PG', 124-125, 'E', 127-139 <MAG>

A:Note: some carboxyl-terminal heterogeneity was found

C:Genetics:

A:Introns: 5/3; 61/3

C:Superfamily: pituitary glycoprotein hormone beta chain

C:Keywords: blocked amino end; glycoprotein; hormone; pituitary

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-141/Product: lutropin beta #status experimental <LTB>

F:21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #stat

F:29-54,43-77,46-108,58-130,92-120,110-113/disulfide bonds: #status predicted

F:33/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 71.28; Score 37; DB 1; Length 141;

Best Local Similarity 60.08; Pred. No. 9.7;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10

||:|||

Db 68 ILPPMPQVVC 77

RESULT 7

UTSHB

Lutropin beta chain precursor - sheep

N:Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 24-Apr-1984 #sequence_revision 19-Jan-2001 #text_change 19-Jan-2001

C:Accession: I46949; S09232; A92110; A90053; B61098; A01500

R:Brown, P.; McNeilly, J.R.; Wallace, R.M.; McNeilly, A.S.; Clark, A.J.

Mol. Cell. Endocrinol. 93, 157-165, 1993

A:Title: Characterization of the ovine LH beta-subunit gene: the promoter directs gonad

A:Reference number: I46949; MUID:93351742; PMID:8349025

A:Accession: I46949

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-141 <BRO>

A:Cross-references: GB:S64695; NID:g408240; PIDN:AAB27819.1; PID:g408241

R:d'Angelo-Bernard, G.; Moumni, M.; Jutisz, M.; Counis, R.

Nucleic Acids Res. 18, 2175, 1990

A:Title: Cloning and sequence analysis of the cDNA for the precursor of the beta subu

A:Reference number: S09232; MUID:90245669; PMID:2336396

A:Accession: S09232

A:Molecule type: mRNA

A:Residues: 1-56, 'L', 60-62, 'Q', 64-141 <ANG>

A:Cross-references: EMBL:X52488; NID:g1319; PIDN:CRAA36729.1; PID:g1320

R:Li, W.K.; Nahm, H.S.; Sweeney, C.M.; Holcomb, G.N.; Ward, D.N.

J. Biol. Chem. 247, 4365-4381, 1972

A:Title: The primary structure of ovine luteinizing hormone. II. The amino acid sequ

A:Reference number: A92110; MUID:72211145; PMID:4556309

A:Accession: A92110

A:Molecule type: protein

A:Residues: 21-121, 'PG', 124-125, 'E', 127-139 <LIU>

R:Sairam, M.R.; Samy, T.S.A.; Papkoff, H.; Li, C.H.

Arch. Biochem. Biophys. 153, 572-586, 1972

A:Title: The primary structure of ovine interstitial cell-stimulating hormone. II. Th

A:Reference number: A90053; MUID:73190035; PMID:4575435

A:Accession: A90053

A:Molecule type: protein

A:Residues: 21-29, 'E', 31-71, 'P', 72-80, 'Q', 82-121, 'PG', 124-125, 'E', 127-139 <SAI>

R:Nomura, K.; Tsunasawa, S.; Ohmura, K.; Sakiyama, F.; Shizume, K.

Endocrinology 123, 700-712, 1988

A:Title: Renotropic activity in ovine luteinizing hormone isoform(s).

A:Reference number: A61098; MUID:88283534; PMID:2456202

A:Accession: B61098

A:Molecule type: protein

A:Residues: 21-39, 'N', 41-49; 64-78, 'V', 80-82; 84-106; 115-121, 'PG', 124-138 <NOM>

A:Note: this form was designated form beta-3; forms beta-1 and beta-2 each lack sever

C:Genetics:

A:Introns: 5/3; 61/3

C:Superfamily: pituitary glycoprotein hormone beta chain

C:Keywords: blocked amino end; glycoprotein; hormone; pituitary

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-141/Product: lutropin beta chain #status experimental <MAT>

F:21/Modified site: blocked amino end (Ser) (in mature form) (partial) (probably acet

F:29-54,43-77,46-108,58-130,92-120,110-113/disulfide bonds: #status predicted

F:33/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match

Best Local Similarity 71.28; Score 37; DB 1; Length 141;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10

||:|||

Db 68 ILPPMPQVVC 77

Query Match

Best Local Similarity 60.08; Pred. No. 9.7;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

C:Species: Gallus gallus (chicken)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Jun-1999

C:Accession: S28050

R:Foos, G.; Grilmm, S.; Klemmner, K.H.

EMBO J. 11, 4619-4629, 1992

A:Title: Functional antagonism between members of the myb family: B-myb inhibits v-my

A:Reference number: S28050; MUID:93049214; PMID:1425593

A:Accession: S28050

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-686 <FOO>

A:Cross-references: EMBL:X67505; NID:g63098; PIDN:CAA47839.1; PID:g63099

C:Genetics:

A:Gene: B-myb

C:Function:

A:Description: transcription regulation; widespread activator of cell cycle genes; re

C:Superfamily: myb transforming protein; myb DNA-binding repeat homology

C:Keywords: DNA binding; duplication; nucleus; transcription regulation
 F;26-77/Domain: myb DNA-binding repeat homology <MYB1>
 F;78-129/Domain: myb DNA-binding repeat homology <MYB2>
 F;130-180/Domain: myb DNA-binding repeat homology <MYB3>
 F;392-398/Region: nuclear location signal
 F;552-567/Region: nuclear location signal

Query Match 71.2%; Score 37; DB 1; Length 686;
 Best Local Similarity 55.6%; Pred. No. 48;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LPALPQVVC 10
 :|||:|
 Db 582 MPALPKYIC 590

RESULT 9

T16409

hypothetical protein F48E8.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16409

R:Kirsten, J.

submitted to the EMBL Data Library, March 1995

A:Description: The sequence of C. elegans cosmid F48E8.

A:Reference number: S59413

A:Accession: T16409

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-817 <KIR>

A:Cross-references: EMBL:U23514; NID:g746484; PID:g746490; PIDN:ANC4543.1; CESP:F48E8.6

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:F48E8.6

A:Introns: 107/3; 510/3; 670/3; 733/3

Query Match 71.2%; Score 37; DB 2; Length 817;
 Best Local Similarity 50.0%; Pred. No. 57;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
 :|||:|
 Db 377 VIPMLPRILC 386

RESULT 10

S54594

MSU1 protein - yeast (Saccharomyces cerevisiae)

N:Alternate names: DSS1 protein; probable 3' exoribonuclease component; protein YW8021.1

C:Species: Saccharomyces cerevisiae

C>Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jul-2000

C:Accession: S54594; S48239; S57267; C42461

R:Pearson, D.; Bowman, S.

submitted to the EMBL Data Library, May 1995

A:Reference number: S54582

A:Accession: S54594

A:Molecule type: DNA

A:Residues: 1-969 <PEA>

A:Cross-references: EMBL:Z49704; NID:g825540; PID:g825553; MIPS:YMR287c

A:Experimental source: strain AB972

R:Dmochowska, A.; Golik, P.

submitted to the EMBL Data Library, October 1994

A:Description: The S. cerevisiae MSU1 gene is essential for mitochondrial biogenesis.

A:Reference number: S48239

A:Accession: S48239

A:Molecule type: DNA

A:Residues: 1-221,'R',223-969 <DMO>

A:Cross-references: EMBL:U15461; NID:g557723; PID:g557724

R:Dmochowska, A.; Golik, P.; Stepien, P.P.

Curr. Genet. 28, 108-112, 1995

A:Title: The novel nuclear gene DSS-1 of Saccharomyces cerevisiae is necessary for mitoc

A:Reference number: S57267; MUID:96020155; PMID:8590460

A:Accession: S57267

A:Molecule type: DNA
 A:Residues: 1-221,'R',223-969 <DMW>

A:Cross-references: EMBL:U15461; NID:g557723; PIDN:AA049144.1; PID:g557724

R:Kang, W.; Matsushita, Y.; Grohmann, L.; Graack, H.R.; Kitakawa, M.; Isono, K.

J. Bacteriol. 173, 4013-4020, 1991

A:Title: Cloning and analysis of the nuclear gene for YmlJ33, a protein of the large s

A:Reference number: A42461; MUID:91286184; PMID:2061283

A:Accession: C42461

A:Molecule type: DNA

A:Residues: 804-910,'MV',911-969 <KAN>

A:Cross-references: GB:D90217

A>Note: the authors translated the codon CCA for residue 67 as Thr

C:Genetics:

A:Gene: SGD:MSU1; DSS1

A:Cross-references: SGD:S0004900; MIPS:YMR287c

A:Map position: 13R

A:Genome: nuclear

C:Keywords: mitochondrion

Query Match 71.2%; Score 37; DB 2; Length 969;
 Best Local Similarity 60.0%; Pred. No. 67;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
 :|||:|
 Db 601 VVPMLPQSTIC 610

RESULT 11

T02911

hypothetical protein T13J8.210 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 04-Mar-2000

C:Accession: T02911

R:Bevan, M.; Pohl, T.; Weizenegger, T.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.; Sch

submitted to the Protein Sequence Database, February 1999

A:Reference number: Z14766

A:Accession: T02911

A:Molecule type: DNA

A:Residues: 1-304 <BEV>

A:Cross-references: EMBL:AL035524

A:Experimental source: cultivar Columbia; BAC clone T13J8

C:Genetics:

A:Map position: 4

A:Introns: 198/3

A>Note: T13J8.210

C:Superfamily: Arabidopsis thaliana hypothetical protein T13J8.210

Query Match 69.2%; Score 36; DB 2; Length 304;
 Best Local Similarity 70.0%; Pred. No. 32;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
 :|||:|
 Db 289 VLPFLPLVIC 298

RESULT 12

T19284

hypothetical protein C14H10.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Dec-2000

C:Accession: T19284

R:White, S.

submitted to the EMBL Data Library, August 1995

A:Reference number: Z19102

A:Accession: T19284

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-351 <WIL>

A:Cross-references: EMBL:Z50863; PIDN:CRA90737.1; GSPDB:GN00028; CESP:C14H10.4

A:Experimental source: clone C14H10

C:Genetics:

A:Gene: CESP:C14H10.4
A:Map position: X
A:Introns: 163/2; 316/1
C:Superfamily: Caenorhabditis elegans hypothetical protein C45H4.12

Query Match 69.2%; Score 36; DB 2; Length 351;
Best Local Similarity 60.0%; Pred. No. 38;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLPALPOVVC 10
||||| : : :
Db 258 VLPAPVLLC 267

RESULT 13

T23320 hypothetical protein K04G11.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
C:Accession: T23320; T26015

R:Baynes, C.
submitted to the EMBL Data Library, August 1996

A:Reference number: Z19726
A:Accession: T23320
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-102 <WIL>
A:Cross-references: EMBL:Z78544; PIDN:CAB01763.1; GSPDB:GN00028; CESP:K04G11.6
A:Experimental source: clone K04G11

R:Smey, R.
submitted to the EMBL Data Library, August 1998

A:Reference number: Z20132
A:Accession: T26015
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-102 <WIL>
A:Cross-references: EMBL:AL031265; PIDN:CAA20328.1; GSPDB:GN00028; CESP:K04G11.6
A:Experimental source: clone VK04G11

C:Genetics:
A:Gene: CESP:K04G11.6
A:Map position: X
A:Introns: 43/2

C:Superfamily: Caenorhabditis elegans hypothetical protein K04G11.6

Query Match 67.3%; Score 35; DB 2; Length 102;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLPALPOVVC 10
: || ||| :
Db 72 ILPNLPQNLK 81

RESULT 14

B83612 hypothetical protein PA0274 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B83612
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizioch, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen

A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: B83612
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-256 <STO>
A:Cross-references: GB:AE000465; GB:AE000491; NID:g9946107; PIDN:AAG03663.1; GSPDB:GN0011
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0274

Query Match 67.3%; Score 35; DB 2; Length 256;
Best Local Similarity 75.0%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PALPOVVC 10
||||| : :
Db 4 PALPAVLC 11

RESULT 15

AE0094 probable gluconate transporter gntP [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AE0094

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; M., M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AE0001; MUID:21470413; PMID:11586360

A:Accession: AE0094
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-447 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC89616.1; PID:gl5978845; GSPDB:GN00175
C:Genetics:
A:Gene: gntP
C:Superfamily: D-serine permease

Query Match 67.3%; Score 35; DB 2; Length 447;
Best Local Similarity 60.0%; Pred. No. 74;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLPALPOVVC 10
|| ||| : :
Db 182 VLVAIPSVIC 191

RESULT 16

I65981 fatty acid omega-hydroxylase (EC 1.14.15.-) cytochrome P450 4A11 - human

C:Species: Homo sapiens (man)
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 04-Mar-2000
C:Accession: I65981
R:Imacka, S.; Ogawa, H.; Kimura, S.; Gonzalez, F.J.
DNA Cell Biol. 12, 893-899, 1993

A:Title: Complete cDNA sequence and cDNA-directed expression of CYP4A11, a fatty acid hydroxylase

A:Reference number: I53015; MUID:94099889; PMID:8274222
A:Accession: I65981
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-591 <RES>

A:Cross-references: GB:S67581; NID:g456997; PIDN:AAB29503.1; PID:g456998

C:Genetics:
A:Gene: GDB:CYP4A11
A:Cross-references: GDB:I38467; OMIM:601310
A:Map position: lpter-lqter

C:Superfamily: human cytochrome P450 CYP4B1: cytochrome P450 homology
C:Keywords: chromoprotein; electron transfer; fatty acid oxidation; heme; iron; metal binding site; heme iron (Cys) (axial ligand) #status predicted
F:457/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 67.3%; Score 35; DB 2; Length 591;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPALPOVVC 10
||||| :
Db 554 LPAPQVAC 562

RESULT 17

H71503
probable fad-dependent oxidoreductase - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 26-Aug-1999
C:Accession: H71503
R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
A:Reference number: A71570; MUID:99000809; PMID:9784136
A:Accession: H71503
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-610 <ARN>
A:Cross-references: GB:AE001323; GB:AE001273; NID:g3328931; PIDN:AAC68099.1; PID:g3328931
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: gidA
C:Superfamily: gidA protein

Query Match 67.3%; Score 35; DB 2; Length 610;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPALPQVVC 10
: | | | | |
Db 235 VPTLPQVSC 243

RESULT 18

I65235
testicular luteinizing hormone beta subunit - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C:Accession: I65235
R:Zhang, F.P.; Rannikko, A.; Huhtaniemi, I. Biochem. Biophys. Res. Commun. 210, 858-865, 1995
A:Title: Isolation and characterization of testis-specific cDNAs for luteinizing hormone
A:Reference number: I52320; MUID:95283549; PMID:7763258
A:Accession: I65235
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-80 <RES>
A:Cross-references: EMBL:U25803; NID:g904025; PIDN:AAC52251.1; PID:g904026
C:Genetics:
A:Gene: TLHB3
C:Superfamily: pituitary glycoprotein hormone beta chain

Query Match 65.4%; Score 34; DB 2; Length 80;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPALPQVVC 10
: | | | | |
Db 9 LPPVPQVVC 17

RESULT 19

A61465
lutropin beta chain - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 08-Dec-1995
C:Accession: A61465
R:Glenn, S.D.; Nahm, H.S.; Ward, D.N. J. Protein Chem. 3, 259-273, 1984
A:Title: The amino acid sequence of the rabbit lutropin beta subunit.
A:Reference number: A61465
A:Accession: A61465
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-119 <GLE>
A:Note: the sequence from Fig. 1 is inconsistent with that from the abstract in having 1
C:Superfamily: pituitary glycoprotein hormone beta chain

F:11-36,25-59,28-90,40-112,74-102,92-95/Disulfide bonds: #status predicted
Query Match 65.4%; Score 34; DB 2; Length 119;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPALPQVVC 10
: | | | | |
Db 51 LPPVPQVVC 59

RESULT 20

S00512
lutropin beta chain precursor - dog (fragment)
N:Alternate names: luteinizing hormone beta chain
C:Species: Canis lupus familiaris (dog)
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999
C:Accession: S00512
R:Wolf, D.L.; Appleby, V.L.; Hjerrild, K.; Baker, A.R.; Talmadge, K. Nucleic Acids Res. 15, 10602, 1987
A:Title: Nucleic acid and amino acid sequences of dog beta-LH: comparison to rat, cow
A:Reference number: S00512; MUID:88096605; PMID:3697104
A:Accession: S00512
A:Molecule type: mRNA
A:Residues: 1-138 <WOL>
A:Cross-references: EMBL:Y00518; NID:g907; PIDN:CAA68572.1; PID:g860906
C:Superfamily: pituitary glycoprotein hormone beta chain
F:1-17/Domain: signal sequence (fragment) #status predicted <SIG>
F:18-138/Product: lutropin beta chain #status predicted <MAT>
F:26-51,40-74,43-105,55-127,89-117,107-110/Disulfide bonds: #status predicted

Query Match 65.4%; Score 34; DB 2; Length 138;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPALPQVVC 10
: | | | | |
Db 66 LPPVPQVVC 74

RESULT 21

I52320
testicular luteinizing hormone beta-subunit - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C:Accession: I52320
R:Zhang, F.P.; Rannikko, A.; Huhtaniemi, I. Biochem. Biophys. Res. Commun. 210, 858-865, 1995
A:Title: Isolation and characterization of testis-specific cDNAs for luteinizing hormone
A:Reference number: I52320; MUID:95283549; PMID:7763258
A:Accession: I52320
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-139 <RES>
A:Cross-references: EMBL:U25653; NID:g915216; PIDN:AAC52249.1; PID:g915217
C:Genetics:
A:Gene: TLHB1
C:Superfamily: pituitary glycoprotein hormone beta chain

Query Match 65.4%; Score 34; DB 2; Length 139;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPALPQVVC 10
: | | | | |
Db 67 LPPVPQVVC 75

RESULT 22

UTRTB
lutropin beta chain precursor - rat
N:Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing hormone (LH) beta chain
C:Species: Rattus norvegicus (Norway rat)

C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 24-Sep-1999
C:Accession: A01498; PQ0091; S42527; I83049
R:Jameson, L.; Chinn, W.W.; Hollenberg, A.N.; Chang, A.S.; Habener, J.F.
J. Biol. Chem. 259, 15474-15480, 1984
A:Title: The gene encoding the beta-subunit of rat luteinizing hormone. Analysis of gene
A:Reference number: A01498; MUID:85080043; PMID:6096374
A:Accession: A01498
A:Molecule type: DNA
A:Residues: 1-141 <TAM>
A:Cross-references: EMBL:J00749; NID:g205175; PIDN:AAA96703.1; PID:g205176
R:Kato, Y.; Ezashi, T.; Hirai, T.; Kato, T.
Submitted to JIPID, July 1990
A:Reference number: PQ0091
A:Accession: PQ0091
A:Molecule type: mRNA
A:Residues: 4-141 <KAT>
R:Chin, W.W.; Godine, J.E.; Klein, D.R.; Chang, A.S.; Tan, L.K.; Habener, J.F.
Proc. Natl. Acad. Sci. U.S.A. 80, 4649-4653, 1983
A:Title: Nucleotide sequence of the cDNA encoding the precursor of the beta subunit of
A:Reference number: S42527; MUID:83273673; PMID:6192440
A:Accession: S42527
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-141 <CHI>
A:Cross-references: GB:J00749; GB:M54957; NID:g205175; PIDN:AAA96703.1; PID:g205176
R:Kato, Y.; Ezashi, T.; Hirai, T.; Kato, T.
Zool. Sci. 7, 879-887, 1990
A:Title: Strain Difference in Nucleotide Sequences of Rat Glycoprotein Hormone Subunit
A:Reference number: I60104
A:Accession: I83049
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 4-141 <RES>
A:Cross-references: GB:D00576; NID:g220807; PIDN:BAA00454.1; PID:g220808
C:Comment: The beta chain confers the specificity of the hormone.
C:Genetics:
A:Introns: 5/3; 61/3
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: glycoprotein; hormone; pituitary
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-141/Product: lutropin beta #status predicted <LFB>
F:29-54,43-77,46-108,58-130,92-120,110-113/Disulfide Bonds: #status predicted
F:33/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 65.4%; Score 34; DB 1; Length 141;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 LPALPQVVC 10
DB 69 LPPVPQVVC 77
II :|||
RESULT 23
UTPGB
lutropin beta chain precursor - pig
N:Alternate names: interstitial cell-stimulating hormone (ICSH) beta chain; luteinizing
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 24-Apr-1984 #sequence_revision 30-Jun-1993 #text_change 16-Jun-2000
C:Accession: A48170; A30322; A01501; A60584
R:Ezashi, T.; Hirai, T.; Kato, T.; Wakabayashi, K.; Kato, Y.
J. Mol. Endocrinol. 5, 137-146, 1990
A:Title: The gene for the beta subunit of porcine LH: clusters of GC boxes and CACC ele
A:Reference number: A48170; MUID:91063934; PMID:1701088
A:Accession: A48170
A:Molecule type: DNA
A:Residues: 1-141 <EZA>
A:Cross-references: GB:D00579; NID:g217693; PIDN:BAA00457.1; PID:g217694
R:Kato, Y.; Hirai, T.
Mol. Cell. Endocrinol. 62, 47-53, 1989
A:Title: Cloning and DNA sequence analysis of the cDNA for the precursor of porcine lute
A:Reference number: A30322; MUID:89506142; PMID:2744222
A:Accession: A30322

A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-141 <KAT>
R:Maghain-Rochester, G.; Hennen, G.
Eur. J. Biochem. 39, 235-253, 1973
A:Title: Luteinizing hormone. The primary structures of the beta-subunit from bovine
A:Reference number: A91212; MUID:74075724; PMID:4770795
A:Accession: A01501
A:Molecule type: protein
A:Residues: 21-29,'Z',31-39,'D',41-61,'R',63-82,'I',84-86,'S',88-131,'PG',124-133,'P'
A:Note: 30-Arg was also found
A:Note: about half the chains lack one or both carboxyl-terminal leucines
R:Nomura, K.; Ohmura, K.; Nakamura, Y.; Horiba, N.; Shirakura, Y.; Sato, Y.; Ujihara,
Endocrinology 124, 712-719, 1989
A:Title: Porcine luteinizing hormone isoform(s): relationship between their molecular
A:Reference number: A60584; MUID:89107050; PMID:2536317
A:Accession: A60584
A:Molecule type: protein
A:Residues: 21-31;137-139 <NOM>
A:Note: the lutropin beta chain is heterogeneous at the carboxyl end; this form lacks
C:Genetics:
A:Introns: 5/3; 61/3
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: blocked amino end; glycoprotein; hormone
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-141/Product: lutropin beta chain #status experimental <MAT>
F:21/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #s
F:29-54,43-77,46-108,58-130,92-120,110-113/Disulfide bonds: #status predicted
F:33/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 65.4%; Score 34; DB 1; Length 141;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 LPALPQVVC 10
DB 69 LPPVPQVVC 77
II :|||
RESULT 24
JC4527
luteinizing hormone beta chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 16-Jul-1999
C:Accession: JC4527
R:Kumar, T.R.; Matzuk, M.M.
Gene 166, 335-336, 1995
A:Title: Cloning of the mouse gonadotropin beta-subunit-encoding genes, II. Structure
A:Reference number: JC4527; MUID:96125216; PMID:8543188
A:Accession: JC4527
A:Molecule type: mRNA
A:Residues: 1-141 <KUM>
A:Cross-references: GB:U25145; NID:g930344; PIDN:AAA92841.1; PID:g930345
A:Experimental source: 129SvEv
C:Comment: This protein is co-produced with follicle-stimulating hormone in pituitary
n reproduction including gonadal growth, gametogenesis and steroidogenesis.
C:Genetics:
A:Gene: lh beta
A:Introns: 5/3; 61/3
C:Superfamily: pituitary glycoprotein hormone beta chain
C:Keywords: hormone; reproduction
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-141/Product: luteinizing hormone beta chain #status predicted <MAT>
Query Match 65.4%; Score 34; DB 2; Length 141;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 LPALPQVVC 10
DB 69 LPPVPQVVC 77
II :|||

RESULT 25

D64300
(R)-2-hydroxyglutaryl-CoA dehydratase activator homolog - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: D64300
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8688087
A:Accession: D64300
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-243 <BUL>
A:Cross-references: GB:U67459; GB:L77117; NID:g2826236; PIDN:AAB97985.1; PID:g1590817; T
C:Genetics:
A:Map position: FOR5378-6109
C:Superfamily: hgdC protein

Query Match 65.4%; Score 34; DB 2; Length 243;
Best Local Similarity 50.0%; Pred. No. 62;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
DB 227 LIPKEPQIVC 236

Search completed: December 4, 2002, 11:27:19
Job time : 11 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: December 4, 2002, 11:23:34 ; Search time 5 Seconds
(without alignments)
82.953 Million cell updates/sec

Title: US-09-821-380-3
Perfect score: 52
Sequence: 1 VLPALPQVVC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 65 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	165	1 CGHB_HUMAN	P01233 homo sapien
2	47	90.4	141	1 LSHB_HUMAN	P01229 homo sapien
3	44	84.6	165	1 CGHB_PAPAN	P07434 papio anubi
4	40	76.9	164	1 CGHB_CALJA	P51500 callithrix
5	40	76.9	169	1 LSHB_HORSE	P08751 equus caball
6	37	71.2	141	1 LSHB_BOVIN	P04651 bos taurus
7	37	71.2	141	1 LSHB_SHEEP	P01231 ovis aries
8	37	71.2	556	1 GLI_CHICK	P55878 gallus gall
9	37	71.2	686	1 MYBB_CHICK	Q03237 gallus gall
10	37	71.2	817	1 YR86_CAEEL	Q09568 caenorhabdi
11	37	71.2	969	1 MSU1_YEAST	P39112 saccharomyc
12	36	69.2	701	1 CG1_HUMAN	Q13495 homo sapien
13	35	67.3	169	1 LSHB_EQUAS	P19794 equus asinu
14	35	67.3	169	1 LSHB_EQUUB	O46641 equus burch
15	35	67.3	610	1 GIDA_CHLTR	O84506 chlamydia t
16	34	65.4	128	1 LSHB_PHOSU	Q9949 phodopus su
17	34	65.4	138	1 LSHB_CANFA	P18842 canis famil
18	34	65.4	138	1 LSHB_MACRU	O46483 macropus ru
19	34	65.4	141	1 LSHB_MOUSE	O09108 mus musculu
20	34	65.4	141	1 LSHB_MOUSE	P01232 sus scrofa
21	34	65.4	141	1 LSHB_PIG	P01230 rattus norv
22	34	65.4	143	1 LSHB_RAT	O77805 felis silve
23	34	65.4	243	1 Y004_METJA	Q60315 methanococc
24	34	65.4	294	1 CGG1_MOUSE	P51945 mus musculu
25	34	65.4	310	1 SDC1_HUMAN	P18827 homo sapien
26	34	65.4	311	1 SDC1_MOUSE	P18828 mus musculu
27	34	65.4	313	1 SDC1_RAT	P26260 rattus norv
28	34	65.4	350	1 THBE_HUMAN	P58166 homo sapien
29	34	65.4	610	1 GIDA_CHLMO	Q99j23 chlamydia m
30	33	63.5	364	1 GIDA_HUMAN	Q99r23 homo sapien
31	33	63.5	386	1 DCUP_DROVI	O18601 drosophila
32	33	63.5	424	1 HEM1_CHLTE	Q93st4 chlorobium
33	33	63.5	424	1 HEM1_CHLVI	P28462 chlorobium

CGHB_HUMAN	STANDARD;	PRT;	165 AA.
AC	P01233; Q14000; Q13991;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
DT	16-OCT-2001 (Rel. 01, Last annotation update)		
DE	Chorionadotropin beta chain precursor (Chorionic gonadotropin beta subunit) (CG-beta).		
GN	CSB.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=81012134; PubMed=6774259;		
RA	Fiddes J.C., Goodman H.M.;		
RT	"The cDNA for the beta-subunit of human chorionic gonadotropin suggests evolution of a gene by readthrough into the 3'-untranslated region."		
RL	Nature 286:684-687(1980).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=84093590; PubMed=6690982;		
RA	Talmadge K., Vamvakopoulos N.C., Fiddes J.C.;		
RT	"Evolution of the genes for the beta subunits of human chorionic gonadotropin and luteinizing hormone."		
RL	Nature 307:37-40(1984).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=84008141; PubMed=6194155;		
RA	Pollicastro P., Ovitt C.E., Hoshina M., Fukuoka H., Boothby M.R., Boime I.;		
RT	"The beta subunit of human chorionic gonadotropin is encoded by multiple genes."		

ALIGNMENTS

RESULT 1

CGHB_HUMAN	STANDARD;	PRT;	165 AA.
AC	P01233; Q14000; Q13991;		
DT	21-JUL-1986 (Rel. 01, Created)		
DT	21-JUL-1986 (Rel. 01, Last sequence update)		
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OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
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RL	Nature 286:684-687(1980).		
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RP	SEQUENCE FROM N.A.		
RX	MEDLINE=84093590; PubMed=6690982;		
RA	Talmadge K., Vamvakopoulos N.C., Fiddes J.C.;		
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RL	Nature 307:37-40(1984).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=84008141; PubMed=6194155;		
RA	Pollicastro P., Ovitt C.E., Hoshina M., Fukuoka H., Boothby M.R., Boime I.;		
RT	"The beta subunit of human chorionic gonadotropin is encoded by multiple genes."		

P71367	haemophilus
P74528	synechocyst
Q09786	schizosacch
Q0618	arabidopsis
Q10573	caenorhabdi
Q60791	mus musculu
P33088	balaenopter
P25330	physeter ca
O77835	ceratotheri
O46482	trichosurus
P24523	cricketul
P24522	homo sapien
P48316	mus musculu
P48317	rattus norv
P40805	bacillus su
P38044	synechococ
P45691	escherichia
Q00403	homo sapien
P29053	mus musculu
O8Y861	anabaena sp
Q42330	gallus gall
O62743	cercopithec
P56493	cercopithec
P56439	gorilla gor
P51681	homo sapien
O97883	hylobates l
P79436	macaca mula
P56440	pan troglod
P56441	papio hamad
O97881	pongo pygma
O97880	pygathrix b
O97878	trachypithe

J. Biol. Chem. 258:11492-11499(1983).

[4] SEQUENCE OF 1-20.

RP MEDLINE=81117268; PubMed=7462224;

RA Birken S., Fetherston J., Canfield R.E., Boime I.;

RT "The amino acid sequences of the prepeptides contained in the alpha

RT and beta subunits of human choriongonadotropin.";

RT J. Biol. Chem. 256:1616-1823(1981).

[5] SEQUENCE OF 21-165.

RP MEDLINE=75211304; PubMed=1150658;

RA Morgan F.J., Birken S., Canfield R.E.;

RT "The amino acid sequence of human chorionic gonadotropin. The alpha

RT subunit and beta subunit.";

RT J. Biol. Chem. 250:5247-5258(1975).

[6] PRELIMINARY SEQUENCE OF 21-165.

RP MEDLINE=74011267; PubMed=4795659;

RA Carlsen R.B., Bahl O.P., Swaminathan N.;

RT "Human chorionic gonadotropin. Linear amino acid sequence of the beta

RT subunit.";

RT J. Biol. Chem. 248:6810-6827(1973).

[7] SEQUENCE OF 1-5 FROM N.A.

RP MEDLINE=86195987; PubMed=2422163;

RA Policastro P.F., Daniels-McQueen S., Carle G., Boime I.;

RT "A map of the hCG beta-LH beta cluster.";

RT J. Biol. Chem. 261:5907-5916(1986).

[8] PRELIMINARY ASSIGNMENT OF DISULFIDE BONDS.

RP MEDLINE=81215630; PubMed=7240231;

RA Mise T., Bahl O.P.;

RT "Assignment of disulfide bonds in the beta subunit of human chorionic

RT gonadotropin.";

RT J. Biol. Chem. 256:6587-6592(1981).

[9] DISULFIDE BONDS.

RP MEDLINE=90094415; PubMed=1688430;

RA Saccuzzo Beebe J., Mountjoy K., Krzesicki R.F., Perini F.,

RA Raddon R.W.;

RT "Role of disulfide bond formation in the folding of human chorionic

RT gonadotropin beta subunit into an alpha beta dimer assembly-competent

RT form.";

RT J. Biol. Chem. 265:312-317(1990).

[10] STRUCTURE OF CARBOHYDRATES.

RP MEDLINE=92314469; PubMed=1820200;

RA Weisshaar G., Hiyana J., Renwick A.G.C.;

RT "Site-specific N-glycosylation of human chorionic gonadotropin --

RT structural analysis of glycopeptides by one- and two-dimensional LH

RT NMR spectroscopy.";

RL Glycobiology 1:393-404(1991).

[11] X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).

RP MEDLINE=94261179; PubMed=8202136;

RA Lathorn A.J., Harris D.C., Littlejohn A., Lustbader J.W.,

RA Canfield R.E., Machin K.J., Morgan F.J., Isaacs N.W.;

RT "Crystal structure of human chorionic gonadotropin.";

RL Nature 369:455-461(1994).

CC -!- FUNCTION: STIMULATES THE OVARIAN CHORIONIC GONADOTROPIN. IT

CC ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.

CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA

CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,

CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.

CC -!- TISSUE SPECIFICITY: PLACENTA.

CC -!- DEVELOPMENTAL STAGE: MADE BY THE FIRST TRIMESTER PLACENTA.

CC -!- PHARMACEUTICAL: Available under the names Novarel (ferring) and

CC Profasi (Serono).

CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN

CC FAMILY.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC

DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B).
GN LHB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84093590; PubMed=6690982;
RA Talmadge K., Vamvakopoulos N.C., Fiddes J.C.;
RT "Evolution of the genes for the beta subunits of human chorionic
RL gonadotropin and luteinizing hormone.";
RN Nature 307:37-40(1984).
[2]
RP SEQUENCE OF 21-141.
RX MEDLINE=76062547; PubMed=1191677;
RA Sairam M.R., Li C.H.;
RT "Human pituitary lutropin. Isolation, properties, and the complete
RT amino acid sequence of the beta-subunit.";
RL Biochim. Biophys. Acta 412:70-81(1975).
RN [3]
RP PRELIMINARY SEQUENCE OF 21-141.
RX MEDLINE=73090987; PubMed=4685398;
RA Shome B., Parlow A.F.;
RT "The primary structure of the hormone-specific, beta subunit of human
RT pituitary luteinizing hormone (hLH).";
RL J. Clin. Endocrinol. Metab. 36:618-621(1973).
RN [4]
RP PRELIMINARY PARTIAL SEQUENCE.
RX MEDLINE=73221227; PubMed=4719207;
RA Closset J., Hennen G., Lequin R.M.;
RT "Human luteinizing hormone. The amino acid sequence of the
RT subunit.";
RN FEBS Lett. 29:97-100(1973).
RN [5]
RP STRUCTURE OF CARBOHYDRATE.
RX MEDLINE=91122088; PubMed=1991473;
RA Weisshaar G., Hiyama J., Renwick A.G.C., Nimtz M.;
RT "NMR investigations of the N-linked oligosaccharides at individual
RT glycosylation sites of human lutropin.";
RL Eur. J. Biochem. 195:257-268(1991).
RN [6]
RP STRUCTURE BY NMR OF 58-77.
RX MEDLINE=92357029; PubMed=1495492;
RA Keutmann H.T., Hua Q.-X., Weiss M.A.;
RT "Structure of a receptor-binding fragment from human luteinizing
RT hormone beta-subunit determined by [1H]- and [15N]nuclear magnetic
RT resonance spectroscopy.";
RL Mol. Endocrinol. 6:904-913(1992).
RN [7]
RP VARIANT ARG-74.
RX MEDLINE=92085985; PubMed=1727547;
RA Weiss J., Axelrod L., Whitcomb R.W., Harris P.E., Crowley W.F.,
RA Jameson J.L.;
RT "Hypogonadism caused by a single amino acid substitution in the beta
RT subunit of luteinizing hormone.";
RL New Engl. J. Med. 326:179-183(1992).
RN [8]
RP FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -1- TISSUE SPECIFICITY: PITUITARY.
CC -1- DISEASE: DEFECTS IN LHB ARE A CAUSE OF HYPOGONADISM WHICH IS
CC CHARACTERIZED BY INFERTILITY AND PSEUDOHERMAPHRODITISM.
CC -1- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X00264; CAA25067.1; -;
DR EMBL; S71273; AAD14960.1; ALT_SEQ.
DR PIR; A01497; UTHUB.
DR HSSP; P01233; 1XUL.
DR GlycoSuiteDB; P01229; -;
DR Genew; HGNC:6584; LHB.
DR MTM; 152780; -;
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Glycoprotein; Signal; Pseudohermaphroditism;
KW Disease mutation.
FT SIGNAL 1 20 LUTROPIN BETA CHAIN.
FT CHAIN 21 141 BY SIMILARITY.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .).
FT VARIANT 74 74 Q -> R (IN HYPOGONADISM; LACK OF
FT RECEPTOR-BINDING).
FT CONFLICT 39 39 /FTID=VAR_003189.
FT CONFLICT 76 76 E -> Q (IN REF. 2).
FT CONFLICT 132 135 MISSING (IN REF. 2).
FT SEQUENCE 141 AA; 15345 MW; E411766253113F7C CRC64;
SQ
Query Match 90.4%; Score 47; DB 1; Length 141;
Best Local Similarity 90.0%; Pred. No. 0.044;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VLPALPQVVC 10
Db 68 VLPPLPQVVC 77
RESULT 3
CGHB_PAPAN STANDARD; PRT; 165 AA.
AC P07434;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Choriongonadotropin beta chain precursor (Chorionic gonadotropin beta
DE subunit) (CG-beta).
GN CGB.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87106051; PubMed=2433190;
RA Crawford R.J., Tregear G.W., Niall H.D.;
RT "The nucleotide sequences of baboon chorionic gonadotropin
RT beta-subunit genes have diverged from the human.";
RL Gene 46:161-169(1986).
CC -1- FUNCTION: STIMULATES THE OVARIES TO SYNTHESIZE THE STEROIDS THAT
CC ARE ESSENTIAL FOR THE MAINTENANCE OF PREGNANCY.
CC -1- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA

RT "A single gene encodes the beta-subunits of equine luteinizing hormone and chorionic gonadotropin.";
 RL Mol. Endocrinol. 6:951-959(1992).
 RN [2]
 RP SEQUENCE OF 21-169.
 RX MEDLINE=87250476; PubMed=3298239;
 RA Bousfield G.R., Liu W.-K., Sugino H., Ward D.N.;
 RT "Structural studies on equine glycoprotein hormones. Amino acid sequence of equine lutropin beta-subunit.";
 RL J. Biol. Chem. 262:8610-8620(1987).
 RN [3]
 RP SEQUENCE OF 21-169.
 RX MEDLINE=87250475; PubMed=3298238;
 RA Sugino H., Bousfield G.R., Moore W.T. Jr., Ward D.N.;
 RT "Structural studies on equine glycoprotein hormones. Amino acid sequence of equine chorionic gonadotropin beta-subunit.";
 RL J. Biol. Chem. 262:8603-8609(1987).
 RN [4]
 RP PARTIAL SEQUENCE.
 RA Ward D.N., Moore W.T. Jr., Burleigh B.D.;
 RT "Structural studies on equine chorionic gonadotropin.";
 RL J. Protein Chem. 1:263-280(1982).
 RN [5]
 RP STRUCTURE OF CARBOHYDRATES
 RX MEDLINE=90235854; PubMed=2331995;
 RA Damm J.B.L., Haard K., Kamerling J.P., van Dedem G.W.K.,
 RT Vliegenthart J.F.G.;
 RT "Structure determination of the major N- and O-linked carbohydrate chains of the beta subunit from equine chorionic gonadotropin.";
 RL Eur. J. Biochem. 189:175-183(1990).
 RN [6]
 RP O-GLYCOSYLATION.
 RX PubMed=1133668;
 RA Bousfield G.R., Butnev V.Y., Butnev V.Y.;
 RT "Identification of twelve O-glycosylation sites in equine chorionic gonadotropin beta and equine luteinizing hormone beta by solid-phase Edman degradation.";
 RL Biol. Reprod. 64:136-147(2001).
 CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -!- PTM: MICROHETEROGENEITY AT ASN-33. O-GLYCOSYLATION APPEARS TO BE RESPONSIBLE FOR THE BETA SUBUNIT CONTRIBUTION TO THE DIFFERENCE IN LH RECEPTOR-BINDING ACTIVITY BETWEEN LSH-B AND CG-B.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN FAMILY.
 CC -----
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 CC -----
 DR EMBL; S41704; AAB22775.1; --
 DR PIR; A01503; KTHOB.
 DR PIR; A29304; A29304.
 DR PIR; A29305; A29305.
 DR PIR; A41917; A41917.
 DR HSSP; P01233; 1XUL.
 DR GlycoSuiteDB; P08751; --
 DR InterPro; IPR000359; Cys_Knot.
 DR InterPro; IPR002400; GF_CysKnot.
 DR InterPro; IPR001545; Gly_HormoneB.
 DR Pfam; PF00007; Cys_Knot; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR SMART; SM00068; GHB; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 KW Hormone; Glycoprotein; Signal.

FT SIGNAL 1 20
 FT CHAIN 21 169
 FT DISULFID 29 77
 FT DISULFID 43 92
 FT DISULFID 46 130
 FT DISULFID 54 108
 FT DISULFID 58 110
 FT DISULFID 113 120
 FT CARBOHYD 33 33
 FT CARBOHYD 138 138
 FT CARBOHYD 143 143
 FT CARBOHYD 147 147
 FT CARBOHYD 148 148
 FT CARBOHYD 149 149
 FT CARBOHYD 150 150
 FT CARBOHYD 151 151
 FT CARBOHYD 153 153
 FT CARBOHYD 157 157
 FT CARBOHYD 160 160
 FT CARBOHYD 161 161
 FT CARBOHYD 169 169
 SQ SEQUENCE 169 AA; 17865 MW; 1244ADBE843EFIA CRC64;
 Query Match 76.9%; Score 40; DB 1; Length 169;
 Best Local Similarity 77.8%; Pred. No. 1.2;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LPALPQVVC 10
 Db 69 LPAIPQVVC 77
 RESULT 6
 LSHB_BOVIN
 ID LSHB_BOVIN STANDARD; PRT; 141 AA.
 AC P04651;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-OCT-2001 (Rel. 40, Last annotation update)
 DE Lutropin beta chain precursor (luteinizing hormone beta subunit) (LSH-beta) (LSH-B) (LH-B).
 GN LHB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85207729; PubMed=2987241;
 RA Virgin J.B., Silver B.J., Thomson A.R., Nilson J.H.;
 RT "The gene for the beta subunit of bovine luteinizing hormone encodes a gonadotropin mRNA with an unusually short 5'-untranslated region.";
 RL J. Biol. Chem. 260:7072-7077(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85182575; PubMed=3838746;
 RA Maurer R.A.;
 RT "Analysis of several bovine lutropin beta subunit cDNAs reveals heterogeneity in nucleotide sequence.";
 RL J. Biol. Chem. 260:4684-4687(1985).
 RN [3]
 RP SEQUENCE OF 21-139.
 RX MEDLINE=74075724; PubMed=4770795;
 RA Maguin-Rogister G., Hennen G.;
 RT "Luteinizing hormone. The primary structures of the beta-subunit from bovine and porcine species.";
 RL Eur. J. Biochem. 39:235-253(1973).
 CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN, LUTROPIN, FOLLITROPIN AND GONADOTROPIN.

FT DISULFID 54 108 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 113 120
 FT MOD_RES 21 21 BLOCKED.
 FT CARBOHYD 33 33 /FTID-CAR_000046.
 FT VARIANT 138 141 MISSING (IN SOME MOLECULES).
 FT CONFLICT 30 30 Q -> E (IN REF. 4).
 FT CONFLICT 59 59 L -> P (IN REF. 1).
 FT CONFLICT 63 63 R -> Q (IN REF. 2).
 FT CONFLICT 71 71 P -> PP (IN REF. 4).
 FT CONFLICT 81 81 E -> Q (IN REF. 4).
 FT CONFLICT 122 123 GP -> PG (IN REF. 3 AND 4).
 FT CONFLICT 126 126 Q -> E (IN REF. 3 AND 4).
 SQ SEQUENCE 141 AA; 15184 MW; C59EC7C0AA55A9DC CRC64;

Query Match 71.2%; Score 37; DB 1; Length 141;
 Best Local Similarity 60.0%; Pred. No. 3.6;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
 :|| :|| :||
 Db 68 ILPPMPQVVC 77

RESULT 8

GLI_CHICK
 ID GLI_CHICK STANDARD; PRT; 556 AA.
 AC P55878;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Zinc finger protein GLI1 (GLI) (Fragment).
 GN GLI1 OR GLI.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97105842; PubMed=8948590;
 RA Marigo V., Johnson R.L., Vortkamp A., Tabin C.J.;
 RT "Sonic hedgehog differentially regulates expression of GLI and GLI3 during limb development."
 RL Dev. Biol. 180:273-283(1996).
 CC -!- FUNCTION: MAY REGULATE THE TRANSCRIPTION OF SPECIFIC GENES DURING AND DIGITAL DEVELOPMENT. MAY PLAY A ROLE IN CRANIOFACIAL DEVELOPMENT AND DIGITAL DEVELOPMENT, AS WELL AS DEVELOPMENT OF THE CENTRAL NERVOUS SYSTEM AND GASTROINTESTINAL TRACT. IMPLICATED IN THE TRANSDUCTION OF SHH SIGNAL (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- SIMILARITY: BELONGS TO THE GLI FAMILY OF C2H2-TYPE ZINC-FINGER PROTEINS.

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DR EMBL; U60762; AAB51659.1; -.
 DR HSSP; P08151; 2GLI.
 DR InterPro; IPR000822; Znf_C2H2.
 DR Pfam; PF00096; zf-C2H2; 5.
 DR SMART; SM00355; Znf_C2H2; 5.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
 DR PROSITE; PS0157; ZINC_FINGER_C2H2_2; 5.
 KW Zinc-finger; Metal-binding; DNA-binding; Transcription regulation;
 KW Nuclear protein; Repeat.
 DR DOMAIN 247 399 ZINC FINGERS.

FT ZN_FING 247 272 C2H2-TYPE.
 FT ZN_FING 280 307 C2H2-TYPE.
 FT ZN_FING 313 337 C2H2-TYPE.
 FT ZN_FING 343 368 C2H2-TYPE.
 FT ZN_FING 374 399 C2H2-TYPE.
 FT NON_TER 556 556
 SQ SEQUENCE 556 AA; 60215 MW; 722D2AA5A1CA4D98 CRC64;

Query Match 71.2%; Score 37; DB 1; Length 556;
 Best Local Similarity 66.7%; Pred. No. 15;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 LPALPQVVC 10
 :|| :|| :||
 Db 540 LPAIPEPVC 548

RESULT 9

MYBB_CHICK
 ID MYBB_CHICK STANDARD; PRT; 686 AA.
 AC Q03237;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Myb-related protein B (B-Myb).
 GN MYBL2 OR BMYB.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93049214; PubMed=1425593;
 RA Foos G., Grimm S., Klempner K.-H.;
 RT "Functional antagonism between members of the myb family: B-myb inhibits v-myb-induced gene activation."
 RL EMBO J. 11:4619-4629(1992).
 RN [2]
 RP STRUCTURE BY NMR OF 79-186
 RX MEDLINE=98322063; PubMed=9657674;
 RA McIntosh P.B., Frenkel T.A., Wollborn U., McCormick J.E., Klempner K.H., Feeney J., Carr M.D.;
 RT "Solution structure of the B-Myb DNA-binding domain: a possible role for conformational instability of the protein in DNA binding and control of gene expression."
 RL Biochemistry 37:9619-9629(1998).
 CC -!- FUNCTION: IT REPRESSSES V-MYB- AND C-MYB-MEDIATED ACTIVATION OF THE MIM-1 GENE, PROBABLY BY COMPETING WITH OTHER MYB PROTEINS FOR BINDING SITES. IT IS AN INHIBITORY MEMBER OF THE MYB FAMILY.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN HEMATOPOIETIC AND NON HEMATOPOIETIC CELLS.
 CC -!- SIMILARITY: CONTAINS 3 MYB-LIKE DOMAINS.

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DR EMBL; X67505; CAA47839.1; -.
 DR PIR; S28050; S28050
 DR PDB; 1A5J; 01-JUL-98.
 DR TRANSFAC; T01586; -.
 DR InterPro; IPR001005; Myb_DNA_binding.
 DR Pfam; PF00249; myb_DNA-binding; 3.
 DR SMART; SM00395; SANT; 3.
 DR PROSITE; PS00037; MYB_1; 3.
 DR PROSITE; PS00334; MYB_2; 3.
 DR PROSITE; PS00090; MYB_3; 3.

```
KW Transcription regulation; Nuclear protein; DNA-binding; Repeat;
KW 3D-structure.
FT DNA_BIND 26 77 MYB 1.
FT DNA_BIND 78 129 MYB 2.
FT DNA_BIND 130 180 MYB 3.
SQ SEQUENCE 686 AA; 77736 MW; 2D1209EAD6489D7B CRC64;

Query Match 71.2%; Score 37; DB 1; Length 686;
Best Local Similarity 55.6%; Pred. No. 18;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LPALPQVVC 10
:||||:
Db 582 MPALPKTIC 590

RESULT 10
YR86_CAEEL STANDARD; PRT; 817 AA.
AC Q09568;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein F48E8.6 in chromosome III.
GN F48E8.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN K12751;
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Kirsten J.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE RIBONUCLEASE II (RNB) FAMILY.
CC
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CC
CC EMBL; U23514; AAC46543.1; -.
DR WormPep; F48E8.6; CE02758.
DR InterPro; IPR001900; Ribonuclease_II.
DR Pfam; PF00773; RNB; 1.
DR PROSITE; PS01175; RIBONUCLEASE_II; 1.
KW Hypothetical protein; Hydrolase; Nuclease.
SQ SEQUENCE 817 AA; 93727 MW; 9BE5B06162699243 CRC64;

Query Match 71.2%; Score 37; DB 1; Length 817;
Best Local Similarity 50.0%; Pred. No. 22;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
:||||:
Db 377 VIPMLPRILC 386

RESULT 11
MSUL_YEAST STANDARD; PRT; 969 AA.
AC P39112;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Mitochondrial biogenesis MSUL protein.
GN MSUL OR YMR287C OR YMR021.13C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Dmochowska A., Golik P.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Pearson D., Bowman S., Barrell B.G., Rajandream M.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ESSENTIAL FOR MITOCHONDRIAL BIOGENESIS.
CC -!- SIMILARITY: BELONGS TO THE RIBONUCLEASE II (RNB) FAMILY.
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CC
CC EMBL; U15461; AAC49144.1; -.
DR EMBL; Z49704; CAA89785.1; -.
DR PIR; S48239; S48239.
DR SGD; S0004900; MSU1.
DR InterPro; IPR001900; Ribonuclease_II.
DR Pfam; PF00773; RNB; 1.
DR PROSITE; PS01175; RIBONUCLEASE_II; 1.
KW Mitochondrion.
FT CONFLICT 222 222 H -> R (IN REF. 1).
SQ SEQUENCE 969 AA; 110821 MW; EBD898F2DB4EFAZD CRC64;

Query Match 71.2%; Score 37; DB 1; Length 969;
Best Local Similarity 60.0%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
:||||:
Db 601 VVPMPLQSC 610

RESULT 12
CGI_HUMAN STANDARD; PRT; 701 AA.
AC Q13495;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CGI protein (F18).
DE CXORF6 OR CGI.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96225444; PubMed=8640223;
RA Laporte J., Hu L.-J., Kretz C., Mandel J.-L., Kioschis P., Coy J.,
RA Klauk S.M., Poutska A., Dahl N.;
RT "A gene mutated in X-linked myotubular myopathy defines a new
RL putative tyrosine phosphatase family conserved in yeast."
RL Nat. Genet. 13:175-182(1996).
CC -!- TISSUE SPECIFICITY: DIFFERENTIALLY EXPRESSED IN SKELETAL MUSCLE.
CC
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CC
CC EMBL; U46023; AAC50551.1; -.

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DR Genew; HGNC:2568; CXorf6.
 DR MIM; 300120; -.
 FT DOMAIN 275 286 POLY-PRO.
 FT DOMAIN 419 429 POLY-GLN.
 FT DOMAIN 522 533 POLY-GLN.
 SQ SEQUENCE 701 AA; 74475 MW; ADIC18E4F6DFD34E CRC64;
 Query Match 69.2%; Score 36; DB 1; Length 701;
 Best Local Similarity 66.7%; Pred. No. 29;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LPALPQVVC 10
 Db 560 MPALPRQVC 568

RESULT 13
 LSHB_EQUAS
 ID LSHB_EQUAS STANDARD; PRT; 169 AA.
 AC P19794;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Lutropin/choriogonadotropin beta chain precursor (LSH-B/CG-B)
 DE (Lutenizing hormone beta subunit).
 GN LHB.
 OS Equus asinus (Donkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Perissodactyla; Equidae; Equus.
 ON NCBI_TaxID=9793;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chopineau M., Combarneau Y., Allen W.R., Stewart F.;
 RL Submitted (JUL-1994) to the EMBL/GenBank/DBJ databases.
 RP [2]
 RP PRELIMINARY SEQUENCE OF 105-169 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=90262634; PubMed=2344391;
 RA Leigh S.E.A., Stewart F.;
 RT "Partial cDNA sequence for the donkey chorionic gonadotropin-beta
 subunit suggests evolution from an ancestral LH-beta gene.";
 RL J. Mol. Endocrinol. 4:143-150(1990)
 CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
 CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
 CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL; X80116; CAA56422.1; -.
 DR EMBL; X53669; CAA37709.1; ALT_SEQ.
 DR PIR; S15676; S15676.
 DR HSSP; P01233; 1XUL.
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR002400; GF_cysknot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR SMART; SM00068; GHB; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 KW Hormone; Glycoprotein; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 169
 FT LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
 FT BY SIMILARITY.
 FT DISULFID 43 92
 FT DISULFID 46 130
 FT BY SIMILARITY.

FT DISULFID 29 77 BY SIMILARITY.
 FT DISULFID 43 92 BY SIMILARITY.
 FT DISULFID 46 130 BY SIMILARITY.
 FT DISULFID 54 108 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 113 120 BY SIMILARITY.
 FT CARBOHYD 33 N-LINKED (GLCNAC... (PROBABLE).
 SQ SEQUENCE 169 AA; 17943 MW; AEED20891E96FA7C CRC64;
 Query Match 67.3%; Score 35; DB 1; Length 169;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 LPALPQVVC 10
 Db 69 LPPIQPVC 77

RESULT 14
 LSHB_EQUBU
 ID LSHB_EQUBU STANDARD; PRT; 169 AA.
 AC O46641;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lutropin/choriogonadotropin beta chain precursor (LSH-B/CG-B)
 DE (Lutenizing hormone beta subunit).
 GN LHB.
 OS Equus burchelli (Plains zebra) (Equus quagga).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Perissodactyla; Equidae; Equus.
 ON NCBI_TaxID=9790;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RX MEDLINE=99273280; PubMed=10341734;
 RA Chopineau M., Martinat N., Pourchet C., Stewart F., Combarneau Y.,
 RA Guilleou F.;
 RT "Cloning, sequencing and functional expression of zebra (Equus
 burchelli) LH.";
 RL J. Reprod. Fertil. 115:159-166(1999).
 CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
 CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
 CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
 CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
 CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
 CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL; Y16265; CAA76146.1; -.
 DR HSSP; P01233; 1XUL.
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR002400; GF_cysknot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR SMART; SM00068; GHB; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 KW Hormone; Glycoprotein; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 169
 FT LUTROPIN/CHORIOGONADOTROPIN BETA CHAIN.
 FT BY SIMILARITY.
 FT DISULFID 29 77
 FT DISULFID 43 92
 FT DISULFID 46 130
 FT BY SIMILARITY.

```
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 169 AA; 17824 MW; 322DF724AEA93E9 CRC64;

Query Match 67.3%; Score 35; DB 1; Length 169;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPALPQVVC 10
DB 69 LPPIQPVC 77

RESULT 15
GIDA_CHLTR STANDARD; PRT; 610 AA.
AC 084506;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glucose inhibited division protein A.
GN GIDA OR CT498.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UN-3/Cx;
RX MEDLINE=99000809; PubMed=9784136;
RA Stephens R.S.; Kalman S.; Lammel C.J.; Fan J.; Marathe R.; Aravind L.;
RA Mitchell W.P.; Olinger L.; Tatusov R.L.; Zhao Q.; Koonin E.V.;
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
RN [2]
RP SEQUENCE OF 39-80 FROM N.A.
RC Wang L.; Steenburg S.D.; Zheng Y.; Larsen S.H.;
RA STRAIN=L2/434/BU;
RT "Gene identification of Chlamydia trachomatis by random DNA
RT sequencing."
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: NOT KNOWN
CC -!- SIMILARITY: BELONGS TO THE GIDA FAMILY.
-----
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-----
CC EMBL; AF001323; AAC68099.1; -
CC EMBL; AF087351; AAD04123.1; -
CC InterPro; IPR001327; FAD_pyr_redox.
CC InterPro; IPR002218; GIDA.
CC InterPro; IPR004416; GIDA_sub.
CC InterPro; IPR002025; NAD_binding.
CC Pfam; PF01134; GIDA; 1.
CC PRINTS; PR00368; FADPNR.
CC ProDom; PD003738; GIDA; 1.
CC TIGRFAMs; TIGR00136; gida; 1.
CC PROSITE; PS01280; GIDA_1; 1.
CC PROSITE; PS01281; GIDA_2; 1.
CC Complete proteome.
SQ SEQUENCE 610 AA; 67202 MW; 6FF516182E49B49D CRC64;

Query Match 67.3%; Score 35; DB 1; Length 610;
Best Local Similarity 66.7%; Pred. No. 39;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPALPQVVC 10
DB 235 VPTLPQVSC 243

RESULT 16
LSHB_PHOSU STANDARD; PRT; 128 AA.
AC 09QYA9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B) (Fragment).
GN LHB.
OS Phodopus sungorus (Striped hairy-footed hamster) (Djungarian hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Phodopus.
OX NCBI_TaxID=10044;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20078932; PubMed=10611080;
RA Bernard D.J.; Merzlyak I.Y.; Horton T.H.; Turek F.W.;
RT "Differential regulation of pituitary gonadotropin subunit messenger
RT ribonucleic acid levels in photostimulated Siberian hamsters.";
RL Biol. Reprod. 62:155-161(2000).
CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
-----
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or send an email to license@isb-sib.ch).
-----
CC EMBL; AF106915; AAF15966.1; -
CC HSP; P01233; 1XUL.
CC InterPro; IPR000359; Cys_knot.
CC InterPro; IPR002400; GF_cysknot.
CC InterPro; IPR001545; Gly_hormoneB.
CC Pfam; PF00007; Cys_knot; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC SMART; SM00068; GHB; 1.
CC PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
CC PROSITE; PS00689; GLYCO_HORMONE_BETA_2; PARTIAL.
CC Hormone; Signal; Glycoprotein.
CC SIGNAL 1 20 BY SIMILARITY.
CC FT CHAIN 21 >128 LUTROPIN BETA CHAIN.
CC FT DISULFID 29 77 BY SIMILARITY.
CC FT DISULFID 43 92 BY SIMILARITY.
CC FT DISULFID 54 108 BY SIMILARITY.
CC FT DISULFID 58 110 BY SIMILARITY.
CC FT DISULFID 113 120 BY SIMILARITY.
CC FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT NON_TER 128 128
CC SEQUENCE 128 AA; 13660 MW; BBF9F655E8E08625 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 128;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPALPQVVC 10
DB 235 VPTLPQVVC 243
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Db 69 LPPVPQVC 77

RESULT 17
LSHB_CANFA
ID LSHB_CANFA STANDARD; PRT; 138 AA.
AC P18942;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B) (Fragment).
GN LHB.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86096605; PubMed=3697104;
RA Wolf D.L., Appleby V.L., Hjerrild K., Baker A.R., Talmadge K.;
RT "Nucleic acid and amino acid sequences of dog beta LH: comparison to
RT rat, cow and human beta LH.";
RL Nucleic Acids Res. 15:10602-10602(1987)
CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y00518; CRA68572.1; -.
CC PIR; S00512; S00512.
CC HSSP; P01233; 1XUL.
CC InterPro; IPR000359; Cys_knot.
CC InterPro; IPR001545; Gly_hormoneB.
CC Pfam; PF00007; Cys_knot; 1.
CC SMART; SM00068; GHb; 1.
CC PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
CC PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
CC Hormone; Signal; Glycoprotein.
CC NON_TER 1
CC SIGNAL <1 17
CC CHAIN 18 138
CC LUTROPIN BETA CHAIN.
CC BY SIMILARITY.
CC DISULFID 26 74
CC BY SIMILARITY.
CC DISULFID 40 89
CC BY SIMILARITY.
CC DISULFID 43 127
CC BY SIMILARITY.
CC DISULFID 51 105
CC BY SIMILARITY.
CC DISULFID 55 107
CC BY SIMILARITY.
CC DISULFID 110 117
CC BY SIMILARITY.
CC CARBOHYD 30 30
CC N-LINKED (GLCNAC... ) (PROBABLE).
CC SEQUENCE 138 AA; 14594 MW; E3639FE6B03F1948 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 138;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 LPALPQVC 10
Db 66 LPPVPQVC 74

RESULT 18
LSHB_MACRO
ID LSHB_MACRO STANDARD; PRT; 138 AA.
AC P18942;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B) (Fragment).
GN LHB.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86096605; PubMed=3697104;
RA Wolf D.L., Appleby V.L., Hjerrild K., Baker A.R., Talmadge K.;
RT "Nucleic acid and amino acid sequences of dog beta LH: comparison to
RT rat, cow and human beta LH.";
RL Nucleic Acids Res. 15:10602-10602(1987)
CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Y00518; CRA68572.1; -.
CC PIR; S00512; S00512.
CC HSSP; P01233; 1XUL.
CC InterPro; IPR000359; Cys_knot.
CC InterPro; IPR001545; Gly_hormoneB.
CC Pfam; PF00007; Cys_knot; 1.
CC SMART; SM00068; GHb; 1.
CC PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
CC PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
CC Hormone; Signal; Glycoprotein.
CC NON_TER 1
CC SIGNAL <1 17
CC CHAIN 18 138
CC LUTROPIN BETA CHAIN.
CC BY SIMILARITY.
CC DISULFID 26 74
CC BY SIMILARITY.
CC DISULFID 40 89
CC BY SIMILARITY.
CC DISULFID 43 127
CC BY SIMILARITY.
CC DISULFID 51 105
CC BY SIMILARITY.
CC DISULFID 55 107
CC BY SIMILARITY.
CC DISULFID 110 117
CC BY SIMILARITY.
CC CARBOHYD 30 30
CC N-LINKED (GLCNAC... ) (PROBABLE).
CC SEQUENCE 138 AA; 14594 MW; E3639FE6B03F1948 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 138;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 LPALPQVC 10
Db 66 LPPVPQVC 74

RESULT 19
LSHB_MOUSE
ID LSHB_MOUSE STANDARD; PRT; 141 AA.
AC O09108; Q60844;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

```

DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B).
GN LHB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=96125216; PubMed=8543189;
RA Kumar T.R., Matzuk M.M.;
RT "Cloning of the mouse gonadotropin beta-subunit-encoding genes, II.
RT Structure of the luteinizing hormone beta-subunit-encoding genes.";
RL Gene 166:335-336(1995).
RN [2]
RP SEQUENCE OF 18-122 FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=Anterior pituitary;
RA Brown P., Brooks J., McNeilly J.R., McNeilly A.S.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U25145; AAA92841.1; -;
DR EMBL; Y10418; CAA71445.1; -;
DR HSSP; P01233; 1XUL.
DR MGI; 96782; Lhb.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Signal; Glycoprotein.
FT SIGNAL 1 20
FT CHAIN 21 141 LUTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 83 83 A -> R (IN REF. 2).
SQ SEQUENCE 141 AA; 15028 MW; 55997CABF3D90BF CRC64;

Query Match Similarity 65.4%; Score 34; DB 1; Length 141;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPALPQWVC 10
DQ 69 LPVPQWVC 77
II -II II

RESULT 20
LSHB_PIG STANDARD; PRT; 141 AA.
ID LSHB_PIG
AC P01232;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B).
GN LHB.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=91063934; PubMed=1701088;
RA Ezashi T., Hirai T., Kato T., Wakabayashi K., Kato Y.;
RT "The gene for the beta subunit of porcine LH: clusters of GC boxes
RT and CACCC elements.";
RL J. Mol. Endocrinol. 5:137-146(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=89306142; PubMed=2744222;
RA Kato Y., Hirai T.;
RT "Cloning and DNA sequence analysis of the cDNA for the precursor of
RT porcine luteinizing hormone (LH) beta subunit.";
RL Mol. Cell. Endocrinol. 62:47-53(1989).
RN [3]
RP SEQUENCE OF 21-139.
RC MEDLINE=74075724; PubMed=4770795;
RA Maghain-Rogister G., Hennen G.;
RT "Luteinizing hormone. The primary structures of the beta-subunit from
RT bovine and porcine species.";
RL Eur. J. Biochem. 39:235-253(1973).
CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERS BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC
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CC
CC EMBL; D00579; BAA00457.1; -;
DR PIR; A30322; UTPGB.
DR PIR; A48170; A48170.
DR HSSP; P01233; 1XUL.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Signal; Glycoprotein.
FT SIGNAL 1 20
FT CHAIN 21 141 LUTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC...).
FT MOD_RES 21 21 BLOCKED.
FT VARIANT 30 30 R -> Z.
FT CONFLICT 40 40 N -> D (IN REF. 3).
FT CONFLICT 62 62 V -> R (IN REF. 3).
FT CONFLICT 83 83 S -> I (IN REF. 3).
FT CONFLICT 87 87 I -> S (IN REF. 3).

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FT CONFLICT 122 123 GP -> PG (IN REF. 3).
SQ SEQUENCE 141 AA: 14889 MW: 803E8E7C59F3C2CF CRC64;

Query Match 65.4%; Score 34; DB 1; Length 141;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPALPQVVC 10
DB 69 LPPVPQVVC 77

RESULT 21
LSHB_RAT
ID LSHB_RAT STANDARD; PRT; 141 AA.
AC P01230;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B).
GN LHB.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=83273673; PubMed=6192440;
RA Chin W.W., Godine J.E., Klein D.R., Chang A.S., Tan L.K.,
RA Habener J.F.;
RT "Nucleotide sequence of the cDNA encoding the precursor of the beta
RT subunit of rat lutropin."
RL Proc. Natl. Acad. Sci. U.S.A. 80:4649-4653(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85080043; PubMed=6096374;
RA Jameson L., Chin W.W., Hollenberg A.N., Chang A.S., Habener J.F.;
RA "The gene encoding the beta-subunit of rat luteinizing hormone."
RT Analysis of gene structure and evolution of nucleotide sequence."
RL J. Biol. Chem. 259:15474-15480(1984).
RN [3]
RP SEQUENCE OF 4-141 FROM N.A.
RC STRAIN=Wistar Imamichi; TISSUE=Anterior pituitary;
RA Kato Y., Ezashi T., Hirai T., Kato T.;
RT "Strain difference in nucleotide sequences of rat glycoprotein hormone
RT subunit cDNAs and gene fragment."
RL Zool. Sci. 7:877-885(1990).
CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERES BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC
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CC
CC EMBL; V01542; CAA24783.1; -
CC EMBL; J00749; BAA96703.1; -
CC EMBL; D00576; BAA0454.1; -
CC PIR; A01498; UTRTB.
CC PIR; S42527; S42527.
CC HSSP; P01233; 1XUL.
CC InterPro; IPR000359; Cys_knot.
CC InterPro; IPR002400; GF_cysknot.
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DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
KW Hormone; Signal; Glycoprotein.
FT SIGNAL 1 20
FT CHAIN 21 141 LUTROPIN BETA CHAIN.
FT DISULFID 29 77 BY SIMILARITY.
FT DISULFID 43 92 BY SIMILARITY.
FT DISULFID 46 130 BY SIMILARITY.
FT DISULFID 54 108 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 113 120 BY SIMILARITY.
FT CARBOHYD 33 33 N-LINKED (GLCNAC... (PROBABLE).
SQ SEQUENCE 141 AA: 15177 MW: 50796F8E32F83BF CRC64;

Query Match 65.4%; Score 34; DB 1; Length 141;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPALPQVVC 10
DB 69 LPPVPQVVC 77

RESULT 22
LSHB_FELCA
ID LSHB_FELCA STANDARD; PRT; 143 AA.
AC 077805;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lutropin beta chain precursor (Luteinizing hormone beta subunit) (LSH-
DE beta) (LSH-B) (LH-B).
GN LHB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary;
RA Pukazhenthi B.S., Varma G.M., Brown J.L.;
RT "Molecular cloning and sequence analysis of the cDNA for the feline
RT luteinizing hormone beta subunit."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROMOTES SPERMATOGENESIS AND OVULATION BY STIMULATING
CC THE TESTES AND OVARIES TO SYNTHESIZE STEROIDS.
CC -!- SUBUNIT: HETERODIMER OF A COMMON ALPHA CHAIN AND A UNIQUE BETA
CC CHAIN WHICH CONFERES BIOLOGICAL SPECIFICITY TO THYROTROPIN,
CC LUTROPIN, FOLLITROPIN AND GONADOTROPIN.
CC -!- SIMILARITY: BELONGS TO THE GLYCOPROTEIN HORMONES BETA CHAIN
CC FAMILY.
CC
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CC
CC EMBL; AF095716; AAC64196.1; -
CC HSSP; P01233; 1XUL.
CC InterPro; IPR000359; Cys_knot.
CC InterPro; IPR002400; GF_cysknot.
CC InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; 1.
```

0;

Gaps

Indels

Mismatches

Conservative

Matches

QY

Db

1

VLPALPQVVC

10

227

LIPKEPQIVC

236

CGGI_MOUSE

STANDARD;

PRT;

294

AA.

RESULT 24

CGGI_MOUSE

ID

AC

P51945; 054779;

DT

01-OCT-1996 (Rel. 34; Created)

DT

01-NOV-1997 (Rel. 35; Last sequence update)

DT

16-OCT-2001 (Rel. 40; Last annotation update)

DE

Cyclin G1 (Cyclin G).

GN

CCNG1 OR CCNG.

OS

Mus musculus (Mouse).

OC

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC

Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

OX

NCBI_TaxID=10090;

RN

[1]

SEQUENCE FROM N.A.

RC

TISSUE=Blood;

RX

MEDLINE=96198057; PubMed=8626390;

RA

Horne M.C., Goolsby G.L., Donaldson K.L., Tran D., Neubauer M.,

RA

Wahl A.F.;

RT

"Cyclin G1 and cyclin G2 comprise a new family of cyclins with

RT

contrasting tissue-specific and cell cycle-regulated expression."

RL

J. Biol. Chem. 271:6050-6061(1996).

RN

[2]

SEQUENCE OF 46-294 FROM N.A.

RP

MEDLINE=95045372; PubMed=7957050;

RX

Okamoto K., Beach D.;

RA

"Cyclin G is a transcriptional target of the p53 tumor suppressor

RT

protein."

RL

EMBO J. 13:4816-4822(1994).

RN

[3]

SEQUENCE FROM N.A.

RP

STRAIN=129;

RX

MEDLINE=98110587; PubMed=9441755;

RA

Kimura S.H., Kataoka T.R., Endo Y., Nojima H.;

RT

"Genomic structure and chromosomal localization of mouse cyclin G1

RT

gene."

RL

Genomics 46:483-486(1997).

RN

[4]

FUNCTION.

RP

MEDLINE=97042488; PubMed=8887688;

RX

Okamoto K., Kamibayashi C., Serrano M., Prives C., Mumby M.C.,

RA

Beach D.;

RT

"p53-dependent association between cyclin G and the B' subunit of

RT

protein phosphatase 2A."

RL

Mol. Cell. Biol. 16:6593-6602(1996).

RN

[5]

FUNCTION, AND SUBCELLULAR LOCATION.

RP

MEDLINE=98359193; PubMed=9696022;

RX

Jensen M.R., Factor V.M., Thorgeirsson S.S.;

RT

"Regulation of cyclin G1 during murine hepatic regeneration following

RT

Dipin-induced DNA damage."

RL

Hepatology 28:537-546(1998).

RN

CC

-1- FUNCTION: MAY PLAY A ROLE IN GROWTH REGULATION. IS ASSOCIATED WITH

CC

G2/M PHASE ARREST IN RESPONSE TO DNA DAMAGE. MAY BE AN

CC

INTERMEDIATE BY WHICH P53 MEDIATES ITS ROLE AS AN INHIBITOR OF

CC

CELLULAR PROLIFERATION.

CC

-1- SUBUNIT: BINDS TO B' REGULATORY B SUBUNITS OF PROTEIN PHOSPHATASE

CC

A (PP2A) FOLLOWING INDUCTION BY P53 (IN VITRO).

CC

-1- SUBCELLULAR LOCATION: Nuclear.

CC

-1- TISSUE SPECIFICITY: HIGHEST LEVELS IN KIDNEY, HEART AND SKELETAL

CC

MUSCLE.

CC

-1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. STRONGEST TO OTHER

CC

CYCLINS CIG1.

CC

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CC

EMBL; U67459; AAB97985.1; -

DR

HSSP; P11568; 1HXH.

DR

TIGR; M30004; -

DR

InterPro; IPR002731; ATPase_BadF.

DR

ProDom; PD006344; ATPase_BadF; 1.

DR

TIGRFAMS; TIGR00241; CoA_E_activ; 1.

DR

Hypothetical protein; Complete proteome.

KW

SEQUENCE 243 AA; 26897 MW; 288C4F4190575E53 CRC64;

SQ

Query Match 65.4%; Score 34; DB 1; Length 243;

Best Local Similarity 50.0%; Pred. No. 24;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY

2

LPLPQVVC

10

71

LPVPQVVC

79

CGGI_MOUSE

STANDARD;

PRT;

243

AA.

Query Match 65.4%; Score 34; DB 1; Length 143;

Best Local Similarity 66.7%; Pred. No. 14;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY

2

LPLPQVVC

10

71

LPVPQVVC

79

CGGI_MOUSE

STANDARD;

PRT;

243

AA.

RESULT 23

Y004_METJA

ID

Q60315;

DT

01-NOV-1997 (Rel. 35; Created)

DT

01-NOV-1997 (Rel. 35; Last sequence update)

DT

16-OCT-2001 (Rel. 40; Last annotation update)

DE

Hypothetical protein M30004.

GN

Methanococcus jannaschii.

OS

Archaea; Euryarchaeota; Methanococci; Methanococcales;

OC

Methanocaldococcaceae; Methanocaldococcus.

OX

NCBI_TaxID=2190;

RN

[1]

SEQUENCE FROM N.A.

RP

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

RX

MEDLINE=96337999; PubMed=8688087;

RA

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

RA

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,

RA

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

RA

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

RA

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

RA

Uttarback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

RA

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

RA

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

RT

"Complete genome sequence of the methanogenic archaeon, Methanococcus

RT

jannaschii."

RL

Science 273:1058-1073(1996).

CC

-1- SIMILARITY: A.FERMENTANS ACTIVATOR OF (R)-HYDROXYGLUTARYL-COA

CC

DEHYDRATASE (HGDC), TO E.COLI YJIL AND M.JANNASCHII M30800.

CC

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CC

EMBL; U67459; AAB97985.1; -

DR

HSSP; P11568; 1HXH.

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CC -----
CC EMBL; L49507; AAC42082.1; -
CC EMBL; Z37110; CAA85474.1; -
CC EMBL; AB005559; BAA24492.1; -
CC MGD; MGI:102890; Ccng.
CC InterPro; IPR004366; Cyclin.
CC Pfam; PF00134; cyclin; 1.
CC SMART; SM00385; CYCLIN; 1.
CC PROSITE; PS00292; CYCLINS; FALSE_NEG.
CC Cyclin; Cell cycle; Cell division; Mitosis; Nuclear protein.
CC FT CONFLICT 175 175 D -> G (IN REF. 3).
CC FT CONFLICT 192 198 IIFSKAK -> SYFLRQ (IN REF. 3).
CC SQ SEQUENCE 294 AA; 33902 MW; 09640ADF4E739BAA CRC64;

Query Match 65.4%; Score 34; DB 1; Length 294;
Best Local Similarity 44.4%; Pred. No. 29;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 LPALPQVVC 10

Db 286 LPTIPETIC 294

RESULT 25

SDCL_HUMAN
ID SDCL_HUMAN STANDARD; PRT; 310 AA.
AC P18827; Q96HB7;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Syndecan-1 precursor (SYND1) (CD138 antigen).
GN SDCL OR SOC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibroblast;
RX MEDLINE=92112751; PubMed=1339431;
RA Lories V., Cassiman J.J., van de Berghe H., David G.;
RT "Differential expression of cell surface heparan sulfate
RT proteoglycans in human mammary epithelial cells and lung
RT fibroblasts.";
RL J. Biol. Chem. 267:1116-1122(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RX MEDLINE=90216719; PubMed=2324102;
RA Mali M., Jaakkola P., Arvilomai A.-M., Jalkanen M.;
RT "Sequence of human syndecan indicates a novel gene family of integral
RT membrane proteoglycans.";
RL J. Biol. Chem. 265:6884-6889(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 23-310 FROM N.A.
RX TISSUE=Placenta;
RC MEDLINE=97203193; PubMed=9050911;
RA Kaukonen J., Alanen-Kurki L., Jalkanen M., Palotie A.;
RT "The mapping and visual ordering of the human syndecan-1 and N-myc
RT genes near the telomeric region of chromosome 2p.";
RL Hum. Genet. 99:295-297(1997).
CC -!- FUNCTION: CELL SURFACE PROTEOGLYCAN THAT BEARS BOTH HEPARAN
CC SULFATE AND CHONDROITIN SULFATE AND THAT LINKS THE CYTOSKELETON

CC TO THE INTERSTITIAL MATRIX.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE SYNDECAN FAMILY OF INTEGRAL MEMBRANE
CC PROTEOGLYCANS.

CC -----
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CC -----
CC EMBL; X60306; CAA42851.1; -
CC EMBL; J05392; AAA60605.1; -
CC EMBL; BC008765; AAH08765.1; -
CC EMBL; Z48199; CAA88235.1; -
CC PIR; A35753; A35753.
CC PIR; S16860; S16860.
CC PIR; A41776; A41776.
CC Genew; HGNC:10658; SDCL.
CC MIM; 186355; -
CC InterPro; IPR003585; Neurexin-like.
CC InterPro; IPR001050; Syndecan.
CC Pfam; PF01034; Syndecan; 1.
CC SMART; SM00294; 4.1m; 1.
CC PROSITE; PS00964; SYNDECAN; 1.
CC Proteoglycan; Heparan sulfate; Transmembrane; Glycoprotein; Signal;
CC Antigen.

FT SIGNAL	1	17	POTENTIAL.
FT CHAIN	18	310	SYNDECAN-1.
FT DOMAIN	18	251	EXTRACELLULAR (POTENTIAL).
FT TRANSMEM	252	276	POTENTIAL.
FT DOMAIN	277	310	CYTOPLASMIC (POTENTIAL).
FT CARBOHYD	37	37	O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT CARBOHYD	43	43	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD	45	45	O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT CARBOHYD	47	47	O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT CARBOHYD	206	206	O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT CARBOHYD	216	216	O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
FT SITE	250	251	CLEAVAGE OF ECTODOMAIN (POTENTIAL).
FT CONFLICT	19	19	P -> L (IN REF. 2).
FT CONFLICT	259	259	G -> V (IN REF. 3).
SQ SEQUENCE	310 AA;	32476 MW;	2C7C02DC5BD90FA5 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 310;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PALPQV 9

Db 19 PALPQIV 25

Search completed: December 4, 2002, 11:26:35
Job time : 6 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 4, 2002, 11:24:20 : Search time 17.75 Seconds
(without alignments)
116.083 Million cell updates/sec

Title: US-09-821-380-3
Perfect score: 52
Sequence: 1 VLPALPQVVC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 65 summaries

Database :

SPREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	159	4 Q8WXL4	Q8wxl4 homo sapien
2	52	100.0	159	4 Q8WXL3	Q8wxl3 homo sapien
3	52	100.0	159	4 Q8WXL2	Q8wxl2 homo sapien
4	52	100.0	159	4 Q8WXL1	Q8wxl1 homo sapien
5	52	100.0	159	4 Q8WTL5	Q8wtl5 homo sapien
6	47	90.4	136	4 Q8WXL0	Q8wxl0 homo sapien
7	47	90.4	136	6 Q8WNB8	Q8wnb8 pongo pygma
8	47	90.4	136	6 Q8WNB6	Q8wnb6 presbytis o
9	47	90.4	157	6 Q8WNC7	Q8wnc7 pongo pygma
10	47	90.4	157	6 Q8WNC5	Q8wnc5 pongo pygma
11	47	90.4	157	6 Q8WNC6	Q8wnc6 pongo pygma
12	47	90.4	157	6 Q8WNC4	Q8wnc4 pongo pygma
13	44	84.6	159	6 Q8WNB3	Q8wnb3 colobus gue
14	44	84.6	159	6 Q8WNB1	Q8wnb1 colobus gue
15	44	84.6	159	6 Q8WNB0	Q8wnb0 macaca mula
16	44	84.6	159	6 Q8WNA9	Q8wna9 macaca mula

17	44	84.6	165	6 Q9BEH1	Q9beh1 macaca fasc
18	43	82.7	159	6 Q8WNA8	Q8wna8 macaca mula
19	43	82.7	165	6 Q9BEH2	Q9beh2 macaca fasc
20	42	80.8	156	6 Q8WNA6	Q8wna6 aotus trivi
21	41	78.8	156	6 Q8WNA7	Q8wna7 callicebus
22	40	76.9	157	6 Q8WNC3	Q8wnc3 presbytis o
23	40	76.9	157	6 Q8WNC2	Q8wnc2 presbytis o
24	40	76.9	157	6 Q8WNC1	Q8wnc1 presbytis o
25	40	76.9	157	6 Q8WNB9	Q8wnb9 presbytis o
26	40	76.9	159	6 Q8WNB4	Q8wnb4 colobus gue
27	40	76.9	159	6 Q8WNB2	Q8wnb2 colobus gue
28	38	73.1	273	5 Q9VEJ3	Q9vej3 drosophila
29	38	73.1	2864	2 Q8VUE5	Q8vue5 erwinia chr
30	37	71.2	627	2 Q9RHD2	Q9rhd2 pseudomonas
31	36	69.2	136	6 Q8WNB5	Q8wnb5 colobus gue
32	36	69.2	144	16 Q93JL1	Q93jl1 streptomyce
33	36	69.2	304	10 Q9SUC9	Q9suc9 arabidopsis
34	36	69.2	351	5 Q62060	Q62060 caenorhabdi
35	36	69.2	406	5 Q8T3W6	Q8t3w6 drosophila
36	36	69.2	442	5 Q9VW63	Q9vw63 drosophila
37	36	69.2	474	11 Q61114	Q61114 mus musculu
38	36	69.2	501	12 Q8UZH1	Q8uzh1 cercopithec
39	36	69.2	648	16 Q8XRI9	Q8xri9 ralionia s
40	36	69.2	795	11 Q9DBY0	Q9dby0 mus musculu
41	35	67.3	89	6 Q46618	Q46618 equus zebra
42	35	67.3	89	6 Q46619	Q46619 equus hemio
43	35	67.3	102	5 Q9XTC5	Q9xtc5 caenorhabdi
44	35	67.3	103	10 P93196	P93196 joinvillea
45	35	67.3	104	10 Q39997	Q39997 hordeum vul
46	35	67.3	126	11 Q9CTV0	Q9ctv0 mus musculu
47	35	67.3	165	6 Q9GL37	Q9gl37 macaca mula
48	35	67.3	165	11 Q99P48	Q99p48 mus musculu
49	35	67.3	253	10 Q9LH23	Q9lh23 oryza sativ
50	35	67.3	256	16 Q916L6	Q916l6 pseudomonas
51	35	67.3	393	10 Q9XHB3	Q9xhb3 chusquea ox
52	35	67.3	394	10 Q9XH94	Q9xh94 pariana rad
53	35	67.3	394	10 Q9XH90	Q9xh90 pharus lapp
54	35	67.3	394	10 Q9XH78	Q9xh78 zizania acu
55	35	67.3	397	10 Q9XH87	Q9xh87 puelia cili
56	35	67.3	397	10 Q9XH82	Q9xh82 streptogyna
57	35	67.3	444	16 Q981L7	Q981l7 rhizobium l
58	35	67.3	447	16 Q82HW4	Q82hw4 yersinia pe
59	35	67.3	922	13 Q8UVF2	Q8uvf2 coturnix co
60	35	67.3	2081	12 Q9WAL8	Q9wal8 satsuma dwa
61	35	67.3	2675	2 Q9FB23	Q9fb23 streptomyce
62	34.5	66.3	136	6 Q8WNB7	Q8wnb7 macaca mula
63	34	65.4	80	11 Q63013	Q63013 rattus norv
64	34	65.4	103	4 Q9H1V9	Q9h1v9 homo sapien
65	34	65.4	136	6 Q8WNA5	Q8wna5 tarsius ban

ALIGNMENTS

RESULT 1					
Q8WXL4					
ID	Q8WXL4	PRELIMINARY;	PRT;	159 AA.	
AC	Q8WXL4				
DT	01-MAR-2002 (Tremblrel. 20, Created)				
DT	01-MAR-2002 (Tremblrel. 20, Last sequence update)				
DT	01-JUN-2002 (Tremblrel. 21, Last annotation update)				
DE	Chorionic gonadotropin beta subunit (Fragment).				
GN	CGB.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Maston G.A., Ruvelo M.;				
RT	"Chorionic gonadotropin has a recent origin in primates and an evolutionary history of selection."				
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.				

```
DR EMBL; AF397576; AAL69704.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
DR FT NON_TER 1 159
DR NON_TER 159
SQ SEQUENCE 159 AA; 16909 MW; A598A73CC97B57EE CRC64;

Query Match 100.0%; Score 52; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 63 VLPALPQVVC 72

RESULT 2
Q8WXL3 PRELIMINARY; PRT; 159 AA.
AC Q8WXL3;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397578; AAL69706.1; -.
DR InterPro; IPR000359; Cys_knot.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
DR FT NON_TER 1 159
DR NON_TER 159
SQ SEQUENCE 159 AA; 17006 MW; AFDC4CE2542EC084 CRC64;

Query Match 100.0%; Score 52; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 63 VLPALPQVVC 72

RESULT 3
Q8WXL2 PRELIMINARY; PRT; 159 AA.
AC Q8WXL2;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397578; AAL69706.1; -.
DR InterPro; IPR000359; Cys_knot.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
DR FT NON_TER 1 159
DR NON_TER 159
SQ SEQUENCE 159 AA; 17006 MW; AFDC4CE2542EC084 CRC64;

Query Match 100.0%; Score 52; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 63 VLPALPQVVC 72

RESULT 4
Q8WXL1 PRELIMINARY; PRT; 159 AA.
AC Q8WXL1;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397581; AAL69709.1; -.
DR InterPro; IPR000359; Cys_knot.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
DR FT NON_TER 1 159
DR NON_TER 159
SQ SEQUENCE 159 AA; 16969 MW; 3C969B3C3D2E57FF CRC64;

Query Match 100.0%; Score 52; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 63 VLPALPQVVC 72

RESULT 5
Q8WTL5 PRELIMINARY; PRT; 159 AA.
AC Q8WTL5;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
```

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 RT evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397577; AAL69705.1; -.
 DR EMBL; AF397580; AAL69708.1; -.
 DR InterPro; IPR000359; Cys_knot.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHb; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1 159
 FT SEQUENCE 159 AA; 16944 MW; 246BA938796A1727 CRC64;

Query Match 100.0%; Score 52; DB 4; Length 159;
 Best Local Similarity 100.0%; Pred. No. 0.044;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
 |||||
 Db 63 VLPPLPQVVC 72

RESULT 6

Q8WXL0
 ID Q8WXL0 PRELIMINARY; PRT; 136 AA.

AC Q8WXL0;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Luteinizing hormone beta subunit (Fragment).
 GN LHB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 RT evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397591; AAL69719.1; -.
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHb; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1 159
 FT SEQUENCE 136 AA; 14712 MW; FE5451852A45054E CRC64;

Query Match 90.48; Score 47; DB 4; Length 136;
 Best Local Similarity 90.0%; Pred. No. 0.32;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
 |||||
 Db 63 VLPPLPQVVC 72

RESULT 7

Q8WNB8
 ID Q8WNB8 PRELIMINARY; PRT; 136 AA.

AC Q8WNB8;

DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Luteinizing hormone beta subunit (Fragment).
 GN LHB.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 RT evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397592; AAL69720.1; -.
 DR InterPro; IPR000359; Cys_knot.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHb; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1 136
 FT SEQUENCE 136 AA; 14708 MW; 11F17052CF0DEFB9 CRC64;

Query Match 90.4%; Score 47; DB 6; Length 136;
 Best Local Similarity 90.0%; Pred. No. 0.32;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
 |||||
 Db 63 VLPPLPQVVC 72

RESULT 8

Q8WNB6
 ID Q8WNB6 PRELIMINARY; PRT; 136 AA.

AC Q8WNB6;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Luteinizing hormone beta subunit (Fragment).
 GN LHB.
 OS Presbytis obscura.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
 OC Presbytis.
 OX NCBI_TaxID=78450;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 RT evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397594; AAL69722.1; -.
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHb; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1 136
 FT SEQUENCE 136 AA; 14722 MW; 2EA6300910968492 CRC64;

Query Match 90.4%; Score 47; DB 6; Length 136;
 Best Local Similarity 90.0%; Pred. No. 0.32;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLPALPQVVC 10
 |||||
 Db 63 VLPPLPQVVC 72

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RESULT 9
Q8WNC7
ID Q8WNC7 PRELIMINARY; PRT; 157 AA.
AC Q8WNC7;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397582; AAL69710.1; -.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 16928 MW; 825D27A00EFD4F6 CRC64;

Query Match 90.4%; Score 47; DB 6; Length 157;
Best Local Similarity 90.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 63 VLPPLPQVVC 72

RESULT 10
Q8WNC6
ID Q8WNC6 PRELIMINARY; PRT; 157 AA.
AC Q8WNC6;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397583; AAL69711.1; -.
DR InterPro; IPR000359; Cys_knot.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 16868 MW; 97BD27A014E1D4EC CRC64;

Query Match 90.4%; Score 47; DB 6; Length 157;
Best Local Similarity 90.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 VLPALPQVVC 10
Db 63 VLPPLPQVVC 72

RESULT 11
Q8WNC5
ID Q8WNC5 PRELIMINARY; PRT; 157 AA.
AC Q8WNC5;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397584; AAL69712.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 17027 MW; 8317774E0F4BD4ED CRC64;

Query Match 90.4%; Score 47; DB 6; Length 157;
Best Local Similarity 90.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
Db 63 VLPPLPQVVC 72

RESULT 12
Q8WNC4
ID Q8WNC4 PRELIMINARY; PRT; 157 AA.
AC Q8WNC4;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397585; AAL69713.1; -.
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHb; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 16985 MW; 825D27AC3EFD4F6 CRC64;
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Query Match 90.4%; Score 47; DB 6; Length 157;
Best Local Similarity 90.0%; Pred. No. 0.37;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
DB 63 VLPPLPQVVC 72

RESULT 13

Q8WNB3 ID Q8WNB3 PRELIMINARY; PRT; 159 AA.

AC Q8WNB3; 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 21, Last annotation update)

DE Chorionic gonadotropin beta subunit (Fragment).

GN CGB.

OS Colobus guereza (Black-and-white colobus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae;

OC Colobus.

OX NCBI_TaxID=33548;

RN [1]

RP SEQUENCE FROM N.A.

RA Maston G.A., Ruvolo M.;

RT "Chorionic gonadotropin has a recent origin in primates and an evolutionary history of selection.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF397597; AAL69725.1; -.

DR InterPro; IPR000359; Cys_knot.

DR Pfam; PF00007; Gly_hormoneB.

DR SMART; SM00068; GHB; 1.

DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.

DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.

FT NON_TER 1 159

FT NON_TER 159

SQ SEQUENCE 159 AA; 16942 MW; 26F692957BD09E35 CRC64;

Query Match 84.6%; Score 44; DB 6; Length 159;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
DB 63 VLPPLPQVVC 72

RESULT 14

Q8WNB1 ID Q8WNB1 PRELIMINARY; PRT; 159 AA.

AC Q8WNB1; 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 21, Last annotation update)

DE Chorionic gonadotropin beta subunit (Fragment).

GN CGB.

OS Colobus guereza (Black-and-white colobus monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; Colobinae;

OC Colobus.

OX NCBI_TaxID=33548;

RN [1]

RP SEQUENCE FROM N.A.

RA Maston G.A., Ruvolo M.;

RT "Chorionic gonadotropin has a recent origin in primates and an evolutionary history of selection.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF397599; AAL69727.1; -.

DR InterPro; IPR000359; Cys_knot.

DR InterPro; IPR001545; Gly_hormoneB.

DR Pfam; PF00007; Cys_knot; 1.

DR SMART; SM00068; GHB; 1.

DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.

DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.

FT NON_TER 1 159

FT NON_TER 159

SQ SEQUENCE 159 AA; 17012 MW; 367EDDDCDE7F6005 CRC64;

Query Match 84.6%; Score 44; DB 6; Length 159;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
DB 63 VLPPLPQVVC 72

RESULT 15

Q8WNB0 ID Q8WNB0 PRELIMINARY; PRT; 159 AA.

AC Q8WNB0; 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 21, Last annotation update)

DE Chorionic gonadotropin beta subunit (Fragment).

GN CGB.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;

OC Cercopitheciidae; Macaca.

OX NCBI_TaxID=9544;

RN [1]

RP SEQUENCE FROM N.A.

RA Maston G.A., Ruvolo M.;

RT "Chorionic gonadotropin has a recent origin in primates and an evolutionary history of selection.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF397600; AAL69728.1; -.

DR InterPro; IPR000359; Cys_knot.

DR InterPro; IPR001545; Gly_hormoneB.

DR Pfam; PF00007; Cys_knot; 1.

DR SMART; SM00068; GHB; 1.

DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.

DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.

FT NON_TER 1 159

FT NON_TER 159

SQ SEQUENCE 159 AA; 16853 MW; 7B64051C2F863870 CRC64;

Query Match 84.6%; Score 44; DB 6; Length 159;
Best Local Similarity 80.0%; Pred. No. 1.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
DB 63 VLPPLPQVVC 72

RESULT 16

Q8WNA9 ID Q8WNA9 PRELIMINARY; PRT; 159 AA.

AC Q8WNA9; 20, Created)

DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (TREMBLrel. 21, Last annotation update)

DE Chorionic gonadotropin beta subunit (Fragment).

GN CGB.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;

OC Cercopitheciidae; Macaca.

OX NCBI_TaxID=9544;

RN [1]

RP SEQUENCE FROM N.A.

RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 evolutionary history of selection.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397601; AAL69729.1; -.
 DR InterPro; IPR000359; Cys_knot.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHb; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 159
 SQ SEQUENCE 159 AA; 16915 MW; 9231691ED0D82863 CRC64;
 Query Match 84.6%; Score 44; DB 6; Length 159;
 Best Local Similarity 80.0%; Pred. No. 1.4;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VLPALPQVVC 10
 III :|||||
 Db 63 VLPPVPQVVC 72
 RESULT 17
 Q9BEH1 PRELIMINARY; PRT; 165 AA.
 AC Q9BEH1;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Chorionic gonadotropin beta subunit 2.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-EMBRYONIC TROPHOBLAST;
 RA Wilken J.A., Matsumoto K., Lasley B.L., Bedows E.;
 RT "A Comparison of Chorionic Gonadotropin Expression by Human and
 Macaque Trophoblast Cells.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY026360; AAK08644.1; -.
 DR HSP; P01233; 1XUL.
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHb; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 SQ SEQUENCE 165 AA; 17743 MW; 2F21566B848592471 CRC64;
 Query Match 84.6%; Score 44; DB 6; Length 165;
 Best Local Similarity 80.0%; Pred. No. 1.4;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VLPALPQVVC 10
 III :|||||
 Db 68 VLPPVPQVVC 77
 RESULT 18
 Q8WNA8 PRELIMINARY; PRT; 159 AA.
 AC Q8WNA8;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Chorionic gonadotropin beta subunit (Fragment).
 GN CGB.
 OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an
 evolutionary history of selection.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397602; AAL69730.1; -.
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHb; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 159
 SQ SEQUENCE 159 AA; 17032 MW; 726E29F7A27E5C04 CRC64;
 Query Match 82.7%; Score 43; DB 6; Length 159;
 Best Local Similarity 70.0%; Pred. No. 2.1;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VLPALPQVVC 10
 III :|||||
 Db 63 ILPPVPQVVC 72
 RESULT 19
 Q9BEH2 PRELIMINARY; PRT; 165 AA.
 AC Q9BEH2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Chorionic gonadotropin beta subunit 1.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-EMBRYONIC TROPHOBLAST;
 RA Wilken J.A., Matsumoto K., Lasley B.L., Bedows E.;
 RT "A Comparison of Chorionic Gonadotropin Expression by Human and
 Macaque Trophoblast Cells.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY026359; AAK08643.1; -.
 DR HSP; P01233; 1XUL.
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHb; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; 1.
 SQ SEQUENCE 165 AA; 17711 MW; 280DF602157D9940 CRC64;
 Query Match 82.7%; Score 43; DB 6; Length 165;
 Best Local Similarity 70.0%; Pred. No. 2.2;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VLPALPQVVC 10
 III :|||||
 Db 68 ILPPVPQVVC 77
 RESULT 20
 Q8WNA6 PRELIMINARY; PRT; 156 AA.
 AC Q8WNA6;

DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Aotus trivirgatus (Night monkey) (Douroucoully).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=9505;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397604; AAL69732.1; -;
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1 156
FT NON_TER 156 156
SQ SEQUENCE 156 AA; 16870 MW; 7799AAAI540EA9A7 CRC64;

Query Match 80.8%; Score 42; DB 6; Length 156;
Best Local Similarity 70.0%; Pred. No. 3.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
I:|:|:|:|
Db 63 VMPPLPQLVC 72

RESULT 21

Q8WNA7 PRELIMINARY; PRT; 156 AA.

ID Q8WNA7
AC Q8WNA7;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Callicebus moloch (Dusky titi).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Callicebinae;
OC Callicebus.
OX NCBI_TaxID=9523;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397603; AAL69731.1; -;
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1 156
FT NON_TER 156 156
SQ SEQUENCE 156 AA; 16578 MW; 6EFBD96B513EABE8 CRC64;

Query Match 78.8%; Score 41; DB 6; Length 156;
Best Local Similarity 80.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
I:|:|:|:|
Db 63 VMPPLPQVVC 72

RESULT 22

Q8WNC3 PRELIMINARY; PRT; 157 AA.

ID Q8WNC3
AC Q8WNC3;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Presbytis obscura.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Presbytis.
OX NCBI_TaxID=78450;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397586; AAL69714.1; -;
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1 157
FT NON_TER 157 157
SQ SEQUENCE 157 AA; 16821 MW; E854A1192407AD0F CRC64;

Query Match 76.9%; Score 40; DB 6; Length 157;
Best Local Similarity 70.0%; Pred. No. 7.4;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLPALPQVVC 10
I:|:|:|:|
Db 63 VLPVPVQAVC 72

RESULT 23

Q8WNC2 PRELIMINARY; PRT; 157 AA.

ID Q8WNC2
AC Q8WNC2;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Chorionic gonadotropin beta subunit (Fragment).
GN CGB.
OS Presbytis obscura.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae; Colobinae;
OC Presbytis.
OX NCBI_TaxID=78450;
RN [1]
RP SEQUENCE FROM N.A.
RA Maston G.A., Ruvolo M.;
RT "Chorionic gonadotropin has a recent origin in primates and an
evolutionary history of selection.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF397587; AAL69715.1; -;
DR InterPro; IPR000359; Cys_knot.
DR InterPro; IPR001545; Gly_hormoneB.
DR Pfam; PF00007; Cys_knot; 1.
DR SMART; SM00068; GHB; 1.
DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
FT NON_TER 1 157
FT NON_TER 157 157
SQ SEQUENCE 157 AA; 16773 MW; 17F1B4E17BE57CB3 CRC64;

Query Match 76.9%; Score 40; DB 6; Length 157;
 Best Local Similarity 70.0%; Pred. No. 7.4;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VLPALPQVVC 10
 ||| :|| ||
 Db 63 VLPPVPQAVC 72

RESULT 24

O8WNC1 PRELIMINARY; PRT; 157 AA.
 ID O8WNC1 AC O8WNC1;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Chorionic gonadotropin beta subunit (Fragment).
 GN CGB.
 OS Presbytis obscura.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Presbytis.
 OX NCBI_TaxID=78450;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397588; AAL69716.1; -.
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.
 DR SMART; SM00068; GHB; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 157
 SQ SEQUENCE 157 AA; 16745 MW; 1D49080831C14FOC CRC64;

Query Match 76.9%; Score 40; DB 6; Length 157;
 Best Local Similarity 70.0%; Pred. No. 7.4;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VLPALPQVVC 10
 ||| :|| ||
 Db 63 VLPPVPQAVC 72

RESULT 25

O8WNB9 PRELIMINARY; PRT; 157 AA.
 ID O8WNB9 AC O8WNB9;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Chorionic gonadotropin beta subunit (Fragment).
 GN CGB.
 OS Presbytis obscura.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Presbytis.
 OX NCBI_TaxID=78450;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maston G.A., Ruvolo M.;
 RT "Chorionic gonadotropin has a recent origin in primates and an evolutionary history of selection."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF397590; AAL69718.1; -.
 DR InterPro; IPR000359; Cys_knot.
 DR InterPro; IPR001545; Gly_hormoneB.
 DR Pfam; PF00007; Cys_knot; 1.

DR SMART; SM00068; GHB; 1.
 DR PROSITE; PS00261; GLYCO_HORMONE_BETA_1; UNKNOWN_1.
 DR PROSITE; PS00689; GLYCO_HORMONE_BETA_2; UNKNOWN_1.
 FT NON_TER 1
 FT NON_TER 157
 SQ SEQUENCE 157 AA; 16787 MW; EDF14B8C3B88C7B3 CRC64;

Query Match 76.9%; Score 40; DB 6; Length 157;
 Best Local Similarity 70.0%; Pred. No. 7.4;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VLPALPQVVC 10
 ||| :|| ||
 Db 63 VLPPVPQAVC 72

Search completed: December 4, 2002, 11:28:35
 Job time : 18.75 secs